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(54) Title: MOLECULAR TOXICOLOGY MODELING

(57) Abstract: The present invention is based on the elucidation of the global changes in gene expression and the identification of toxicity markers in tissues or cells exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The invention includes a database of genes characterized by toxin-induced differential expression that is designed for use with microarrays and other solid-phase probes.

MOLECULAR TOXICOLOGY MODELING

RELATED APPLICATIONS

This application is related to U.S. Provisional Applications 60/222,040, 60/244,880, 60/290,029, 60/290,645, 60/292,336, 60/295,798, 60/297,457, 60/298,884 and 60/303,459, all of which are herein incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

The need for methods of assessing the toxic impact of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism has led to the development of procedures which utilize living organisms as biological monitors. The simplest and most convenient of these systems utilize unicellular microorganisms such as yeast and bacteria, since they are most easily maintained and manipulated. Unicellular screening systems also often use easily detectable changes in phenotype to monitor the effect of test compounds on the cell. Unicellular organisms, however, are inadequate models for estimating the potential effects of many compounds on complex multicellular animals, as they do not have the ability to carry out biotransformations to the extent or at levels found in higher organisms.

The biotransformation of chemical compounds by multicellular organisms is a significant factor in determining the overall toxicity of agents to which they are exposed. Accordingly, multicellular screening systems may be preferred or required to detect the toxic effects of compounds. The use of multicellular organisms as toxicology screening tools has been significantly hampered, however, by the lack of convenient screening mechanisms or endpoints, such as those available in yeast or bacterial systems. In addition, previous attempts to produce toxicology prediction systems have failed to provide the necessary modeling information (*eg.* WO0012760, WO0047761, WO0063435, WO0132928A2, WO0138579A2, and the Affymetrix® Rat Tox Chip.

SUMMARY OF THE INVENTION

The present invention is based on the elucidation of the global changes in gene expression in tissues or cells exposed to known toxins, in particular hepatotoxins, as compared to unexposed tissues or cells as well as the identification of individual genes that are differentially expressed upon toxin exposure.

In various aspects, the invention includes methods of predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, and predicting the hepatoxicity of a compound. The invention also includes methods of identifying agents that modulate the onset or progression of a toxic response. Also provided are methods of predicting the cellular pathways that a compound modulates in a cell. The invention includes methods of identifying agents that modulate protein activities.

In a further aspect, the invention provides probes comprising sequences that specifically hybridize to genes in Tables 1-3. Also provided are solid supports comprising at least two of the previously mentioned probes. The invention also includes a computer system that has a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes in Tables 1-3.

DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.* through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression are also associated with the effects of various chemicals, drugs, toxins, pharmaceutical agents and pollutants on an organism or cells. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes after exposure to an agent could lead to tumorgenesis or hyperplastic growth of cells (Marshall, *Cell*, 64: 313-326 (1991); Weinberg, *Science*, 254:1138-1146 (1991)). Thus, changes in the expression levels of particular genes (*e.g.* oncogenes or tumor suppressors) may serve as signposts for the

presence and progression of toxicity or other cellular responses to exposure to a particular compound.

Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are screened for the ability to interact with a major target without regard to other effects the drugs have on cells. These cellular effects may cause toxicity in the whole animal, which prevents the development and clinical use of the potential drug.

The present inventors have examined tissue from animals exposed to the known hepatotoxins which induce detrimental liver effects, to identify global changes in gene expression induced by these compounds. These global changes in gene expression, which can be detected by the production of expression profiles, provide useful toxicity markers that can be used to monitor toxicity and/or toxicity progression by a test compound. Some of these markers may also be used to monitor or detect various disease or physiological states, disease progression, drug efficacy and drug metabolism.

Identification of Toxicity Markers

To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compounds with well characterized toxicity have been conducted by the present inventors to catalogue altered gene expression during exposure *in vivo* and *in vitro*. In the present study, amitryptiline, alpha-naphthylisothiocyante (ANIT), acetaminophen, carbon tetrachloride, cyproterone acetate (CPA), diclofenac, 17α-ethinylestradiol, indomethacin, valproate and WY-14643 were selected as a known hepatotoxins.

The pathogenesis of acute CCl_4 - induced hepatotoxicity follows a well-characterized course in humans and experimental animals resulting in centrilobular necrosis and steatosis, followed by hepatic regeneration and tissue repair. Severity of the hepatocellular injury is also dose-dependent and may be affected by species, age, gender and diet.

Differences in susceptibility to CCl_4 hepatotoxicity are primarily related to the ability of the animal model to metabolize CCl_4 to reactive intermediates. CCl_4-induced hepatotoxicity is dependent on CCl_4 bioactivation to trichloromethyl free radicals by cytochrome P450 enzymes (CYP2E1), localized primarily in centrizonal hepatocytes.

Formation of the free radicals leads to membrane lipid peroxidation and protein denaturation resulting in hepatocellular damage or death.

The onset of hepatic injury is rapid following acute administration of CCl_4 to male rats. Morphologic studies have shown cytoplasmic accumulation of lipids in hepatocytes within 1 to 3 hours of dosing, and by 5 to 6 hours, focal necrosis and hydropic swelling of hepatocytes are evident. Centrilobular necrosis and inflammatory infiltration peak by 24 to 48 hours post dose. The onset of recovery is also evident within this time frame by increased DNA synthesis and the appearance of mitotic figures. Removal of necrotic debris begins by 48 hours and is usually completed by one week, with full restoration of the liver by 14 days.

Increases in serum transaminase levels also parallel CCl_4-induced hepatic histopathology. In male Sprague Dawley (SD) rats, alanine aminotrasferase (ALT) and aspartate aminotransferase (AST) levels increase within 3 hours of CCl_4 administration (0.1, 1,2, 3, 4 mL/kg, ip; 2.5 mL/kg, po) and reach peak levels (approximately 5-10 fold increases) within 48 hours post dose. Significant increases in serum α-glutathione s-transferase (α-GST) levels have also been detected as early as 2 hours after CCl_4 administration (25 μL/kg, po) to male SD rats.

At the molecular level, induction of the growth-related proto-oncogenes, c-fos and c-jun, is reportedly the earliest event detected in an acute model of CCl_4-induced hepatotoxicity (Schiaffonato *et al.* (1997) Liver 17:183-191). Expression of these early-immediate response genes has been detected within 30 minutes of a single dose of CCl_4 to mice (0.05 -1.5 mL/kg, ip) and by 1 to 2 hours post dose in rats (2 mL/kg, po; 5 mL/kg,po) (Schiaffonato *et al.* (1997) Liver 17:183-191 and Hong *et al.*(1997) Yonsei Medical. J. 38:167-177). Similarly, hepatic c-myc gene expression is increased by 1 hour following an acute dose of CCl_4 to male SD rats (5 mL/kg, po) (Hong *et al.*). Expression of these genes following exposure to CCl_4 is rapid and transient. Peak hepatic mRNA levels for c-fos, c-jun, and c-myc, after acute administration of CCl_4 have been reported at 1 to 2 hours, 3 hours, and 1 hour post dose, respectively.

The expression of tumor necrosis factor-α (TNF-α) is also increased in the livers of rodents exposed to CCl_4, and TNF-α has been implicated in initiation of the hepatic repair process. Pre-treatment with anti-TNF-α antibodies has been shown to prevent CCl_4-mediated increases in c-jun and c-fos gene expression, whereas administration of TNF-α

induced rapid expression of these genes (Bruccoleri *et al.*(1997) Hepatol. 25:133-141). Up-regulation of transforming growth factor- β (TGF-β) and transforming growth factor receptors (TBRI-III) later in the repair process (24 and 48 hours after CCl_4 administration) suggests that TGF-β may play a role in limiting the regenerative response by induction of apoptosis (Grasl-Kraupp *et al.* (1998) Hepatol. 28:717-7126).

Acetaminophen is a widely used analgesic that at supratherapeutic doses can be metabolized to *N*-acetyl-*p*-benzoquinone imine (NAPQI) which causes hepatic and renal failure. At the molecular level, until the present invention little was known about the effects of acetominophen.

Amitriptyline is a commonly used antidepressant, although it is recognized to have toxic effects on the liver (*Physicians Desk Reference, 47th ed.*, Medical Economics Co., Inc., 1993; Balkin, U.S. Patent No. 5,656,284) . Nevertheless, amitriptyline's beneficial effects on depression, as well as on sleep and dyspepsia (H. Mertz *et al.*, *Am J Gastroenterol* 93(2):160-165, 1998), migraines (E. Beubler, *Wien Med Wochenschr* 144(5-6):100-101, 1994), arterial hypertension (T. Bobkiewicz *et al.*, *Arch Immunol Ther Exp (Warsz)* 23(4):543-547, 1975) and premature ejaculation (Smith *et al.*, U.S. Patent No. 5,923,341) mandate its continued use.

Differences in susceptibility to amitriptyline toxicity are considered related to differential metabolism. Amitriptyline-induced hepatotoxicity is primarily mediated by development of cholestasis, the condition caused by the failure of the liver to secrete bile, resulting in accumulation in blood plasma of substances normally secreted into bile-bilirubin and bile salts. Cholestasis is also characterized by liver cell necrosis and bile duct obstruction, which leads to increased pressure on the lumenal side of the canalicular membrane and release of enzymes (alkaline phosphatase, 5'-nucleotidase, gammaglutamyl transpeptidase) normally localized on the canalicular membrane. These enzymes also begin to accumulate in the plasma. Typical symptoms of cholestasis are general malaise, weakness, nausea, anorexia and severe pruritis (Cecil Textbook of Medicine, 20th ed., part XII, pp. 772-773, 805-808, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996).

The effects of amitriptyline or phenobarbital (PB) on phospholipid metabolism in rat liver have been studied. In one study, male Sprague-Dawley rats received amitriptyline orally in one dose of 600 mg/kg. PB was given intraperitonially (IP) at a dosage of 80

mg/kg. Animals were sacrificed by decapitation at 6, 12, 18, and 24 hr. The phospholipid level in liver was measured by enzymatic assay and by gas chromatography-mass spectrometry. Both agents caused an increase in the microsomal phosphatidylcholine content. Levels of glycerophosphate acyltransferase (GAT) and phosphatidate cytidylyltransferase (PCT) were slightly affected by amitriptyline but were significantly affected by PB. Levels of phosphatidate phosphohydrolase (PPH) and choline phosphotransferase (CPT) were significantly altered by amitriptyline and by PB (K. Hoshi *et al.*, "Effect of amitriptyline or phenobarbital on the activities of the enzymes involved in rat liver," *Chem Pharm Bull* 38:3446-3448, 1990).

In another experiment, amitriptyline was given orally to male Sprague-Dawley rats (4-5 weeks old) in a single dose of 600 mg/kg. The animals were sacrificed 12 or 24 hours later. This caused a marked increase in δ-aminolevulinic acid (δ-ALA) activity at both time points. Total heme and cytochrome b5 levels were increased but cytochrome P450 (CYP450) content remained the same. The authors concluded that hepatic heme synthesis is increased through prolonged induction of δ-ALA but this may be accounted for by the increases in cytochrome b5 and total heme and not by the CYP450 content (K. Hoshi *et al.*, "Acute effect of amitriptyline, phenobarbital or cobaltous chloride on δ-aminolevulinic acid synthetase, heme oxygenase and microsomal heme content and drug metabolism in rat liver", *Jpn J Pharmacol* 50:289-293, 1989).

Amitriptyline can cause hypersensititivity syndrome, a specific severe idiosyncratic reaction characterized by skin, liver, joint and haematological abnormalities (H.J. Milionis *et al.*, *Postgrad Med* 76(896):361-363, 2000). Amitriptyline has also been shown to cause drug-induced hepatitis, resulting in liver peroxisomes with impaired catalase function (D. De Creaemer *et al.*, *Hepatology* 14(5):811-817, 1991). The peroxisomes are larger in number, but smaller in size and deformed in shape. Using cultured hepatocytes, the cytotoxicity of amitriptyline was examined and compared to other psychotropic drugs (U.A. Boelsterli *et al.*, *Cell Biol Toxicol* 3(3):231-250, 1987). The effects observed were release of lactate dehydrogenase from the cytosol, as well as impairment of biosynthesis and secretion of proteins, bile acids and glycolipids.

Aromatic and aliphatic isothiocyanates are commonly used soil fumigants and pesticides (E. Shaaya *et al.*, *Pesticide Science* 44(3):249-253, 1995; T. Cairns *et al.*, *J Assoc Official Analytical Chemists* 71(3):547-550, 1988). These compounds are also

environmental hazards, however, because they remain as toxic residues in plants, either in their original or in a metabolized form (M. S. Cerny *et al.*, *J Agricultural and Food Chemistry* 44(12):3835-3839, 1996) and because they are released from the soil into the surrounding air (J. Gan *et al.*, *J Agricutural and Food Chemistry* 46(3):986-990, 1998).

Alpha-naphthylthiourea, an amino-substituted form of ANIT, is a known rodenticide whose principal toxic effects are pulmonary edema and pleural effusion, resulting from the action of this compound on pulmonary capillaries. Microsomes from lung and liver release atomic sulfur (Goodman and Gilman's The Pharmacological Basis of Therapeutics, 9th ed., chapter 67, p. 1690, J. G. Hardman *et al.* Eds., McGraw-Hill, New York, NY, 1996).

In one study in rats, ANIT (80 mg/kg) was dissolved in olive oil and given orally to male Wistar rats (180-320g). All animals were fasted for 24 hours before ANIT treatment, and blood and bile excretion were analyzed 24 hours later. Levels of total bilirubin, alkaline phosphatase, serum glutamic oxaloacetic transaminase and serum glutamic pyruvic transaminase were found to be significantly increased, while ANIT reduced total bile flow, all of which are indications of severe biliary dysfunction. This model is used to induce cholestasis with jaundice because the injury is reproducible and dose-dependent. ANIT is metabolized by microsomal enzymes, and a metabolite plays a fundamental role in its toxicity (M. Tanaka *et al.*, "The inhibitory effect of SA3443, a novel cyclic disulfide compound, on alpha-naphthyl isothiocyanate-induced intrahepatic cholestasis in rats," *Clinical and Experimental Pharmacology and Physiology* 20:543-547, 1993).

ANIT fails to produce extensive necrosis, but has been found to produce inflammation and edema in the portal tract of the liver (T.J. Maziasa *et al.*, "The differential effects of hepatotoxicants on the sulfation pathway in rats," *Toxicol Appl Pharmacol* 110:365-373, 1991). Livers treated with ANIT are significantly heavier than control-treated counterparts and serum levels of alanine aminotransferase (ALT), gamma-glutamyl transpeptidase (γ-GTP), total bilirubin, lipid peroxide and total bile acids showed significant increases (Anonymous, "An association between lipid peroxidation and α-naphthylisothiocyanate-induced liver injury in rats," *Toxicol Lett* 105:103-110, 2000).

ANIT-induced hepatotoxicity may also be characterized by cholangiolitic hepatitis and bile duct damage. Acute hepatotoxicity caused by ANIT in rats is manifested as

neutrophil-dependent necrosis of bile duct epithelial cells (BDECs) and hepatic parenchymal cells. These changes mirror the cholangiolitic hepatitis found in humans (D.A. Hill, *Toxicol Sci* 47:118-125, 1999).

Exposure to ANIT also causes liver injury by the development of cholestasis, the condition caused by failure to secrete bile, resulting in accumulation in blood plasma of substances normally secreted into bile, such as bilirubin and bile salts. Cholestasis is also characterized by liver cell necrosis, including bile duct epithelial cell necrosis, and bile duct obstruction, which leads to increased pressure on the lumenal side of the canalicular membrane, decreased canalicular flow and release of enzymes normally localized on the canalicular membrane (alkaline phosphatase, 5'-nucleotidase, gammaglutamyl transpeptidase). These enzymes also begin to accumulate in the plasma. Typical symptoms of cholestasis are general malaise, weakness, nausea, anorexia and severe pruritis (Cecil Textbook of Medicine, 20th ed., part XII, pp. 772-773, 805-808, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996 and D.C. Kossor *et al.*, "Temporal relationship of changes in hepatobiliary function and morphology in rats following α-naphthylisothiocyanate (ANIT) administration," *Toxicol Appl Pharmacol* 119:108-114, 1993).

ANIT-induced cholestatis is also characterized by abnormal serum levels of alanine aminotransferase, aspartic acid aminotransferase and total bilirubin. In addition, hepatic lipid peroxidation is increased, and the membrane fluidity of microsomes is decreased. Histological changes include an infiltration of polymorphonuclear neutrophils and elevated number of apoptotic hepatocytes (J. R. Calvo *et al.*, *J Cell Biochem* 80(4):461-470, 2001). Other known hepatotoxic effects of exposure to ANIT include a damaged antioxidant defense system, decreased activities of superoxide dismutase and catalase (Y. Ohta *et al.* Toxicology 139(3):265-275, 1999), and the release of several proteases from the infiltrated neutrophils, alanine aminotransferase, cathepsin G, elastase, which mediate hepatocyte killing (D. A. Hill *et al.*, Toxicol Appl Pharmacol 148(1):169-175, 1998).

Indomethacin is a non-steroidal antiinflammatory, antipyretic and analgesic drug commonly used to treat rheumatoid arthritis, osteoarthritis, ankylosing spondylitis, gout and a type of severe, chronic cluster headache characterized by many daily occurrences and jabbing pain. This drug acts as a potent inhibitor of prostaglandin synthesis; it inhibits

the cyclooxygenase enzyme necessary for the conversion of arachidonic acid to prostaglandins (PDR 47th ed., Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's The Pharmalogical Basis of Therapeutics 9th ed., J.G. Hardman *et al.* Eds., McGraw Hill, New York, 1996, pp. 1074-1075, 1089-1095; Cecil Textbook of Medicine, 20th ed., part XII, pp. 772-773, 805-808, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996).

The most frequent adverse effects of indomethacin treatment are gastrointestinal disturbances, usually mild dyspepsia, although more severe conditions, such as bleeding, ulcers and perforations can occur. Hepatic involvement is uncommon, although some fatal cases of hepatitis and jaundice have been reported. Renal toxicity can also result, particularly after long-term administration. Renal papillary necrosis has been observed in rats, and interstitial nephritis with hematuria, proteinuria and nephrotic syndrome have been reported in humans. Patients suffering from renal dysfunction risk developing a reduction in renal blood flow, because renal prostaglandins play an important role in renal perfusion.

In rats, although indomethacin produces more adverse effects in the gastrointestinal tract than in the liver, it has been shown to induce changes in hepatocytic cytochrome P450. In one study, no widespread changes in the liver were observed, but a mild, focal, centrilobular response was noted. Serum levels of albumin and total protein were significantly reduced, while the serum level of urea was increased. No changes in creatinine or aspartate aminotransferase (AST) levels were observed (M. Falzon *et al.*, "Comparative effects of indomethacin on hepatic enzymes and histology and on serum indices of liver and kidney function in the rat," *Br J exp Path* 66:527-534, 1985). In another rat study, a single dose of indomethacin has been shown to reduce liver and renal microsomal enzymes, including CYP450, within 24 hours. Histopathological changes were not monitored, although there were lesions in the GI tract. The effects on the liver seemed to be waning by 48 hours (M.E. Fracasso *et al.*, "Indomethacin induced hepatic alterations in mono-oxygenase system and faecal clostridium perfringens enterotoxin in the rat," *Agents Actions* 31:313-316, 1990).

A study of hepatocytes, in which the relative toxicity of five nonsteroidal antiinflammatory agents was compared, showed that indomethacin was more toxic than the others. Levels of lactate dehydrogenase release and urea, as well as viability and

morphology, were examined. Cells exposed to high levels of indomethacin showed cellular necrosis, nuclear pleomorphism, swollen mitochondria, fewer microvilli, smooth endoplasmic reticulum proliferation and cytoplasmic vacuolation (E.M. Sorensen *et al.*, "Relative toxicities of several nonsteroidal antiinflammatory compounds in primary cultures of rat hepatocytes," *J Toxicol Environ Health* 16(3-4);425-440, 1985).

17α-ethinylestradiol, a synthetic estrogen, is a component of oral contraceptives, often combined with the progestational compound norethindrone. It is also used in post-menopausal estrogen replacement therapy (PDR 47th ed., pp. 2415-2420, Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's The Pharmalogical Basis of Therapeutics 9th ed., pp. 1419-1422, J.G. Hardman *et al.* Eds., McGraw Hill, New York, 1996).

The most frequent adverse effects of 17α-ethinylestradiol usage are increased risks of cardiovascular disease: myocardial infarction, thromboembolism, vascular disease and high blood pressure, and of changes in carbohydrate metabolism, in particular, glucose intolerance and impaired insulin secretion. There is also an increased risk of developing benign hepatic neoplasia, although the incidence of this disease is very low. Because this drug decreases the rate of liver metabolism, it is cleared slowly from the liver, and carcinogenic effects, such as tumor growth, may result.

In a recent study, 17α-ethinylestradiol was shown to cause a reversible intrahepatic cholestasis in male rats, mainly by reducing the bile-salt-independent fraction of bile flow (BSIF) (N.R. Koopen *et al.*, "Impaired activity of the bile canalicular organic anion transporter (Mrp2/cmoat) is not the main cause of ethinylestradiol-induced cholestasis in the rat," *Hepatology* 27:537-545, 1998). Plasma levels of bilirubin, bile salts, aspartate aminotransferase (AST) and alanine aminotransferase (ALT) in this study were not changed. This study also showed that 17α-ethinylestradiol produced a decrease in plasma cholesterol and plasma triglyceride levels, but an increase in the weight of the liver after 3 days of drug administration, along with a decrease in bile flow. Further results from this study are as follows. The activities of the liver enzymes leucine aminopeptidase and alkaline phosphatase initially showed significant increases, but enzyme levels decreased after 3 days. Bilirubin output increased, although glutathione (GSH) output decreased. The increased secretion of bilirubin into the bile without affecting the plasma level suggests that the increased bilirubin production must be related to an increased

degradation of heme from heme-containing proteins. Similar results were obtained in another experiment (G. Bouchard *et al.*, "Influence of oral treatment with ursodeoxycholic and tauroursodeoxycholic acids on estrogen-induced cholestasis in rats: effects on bile formation and liver plasma membranes," *Liver* 13:193-202, 1993) in which the livers were also examined by light and electron microscopy. Despite the effects of the drug, visible changes in liver tissue were not observed.

In another study of male rats, cholestasis was induced by daily subcutaneous injections of 17α-ethinylestradiol for five days. Cholestasis was assessed by measuring the bile flow rate. Rats allowed to recover for five days after the end of drug treatment showed normal bile flow rates (Y. Hamada *et al.*, "Hormone-induced bile flow and hepatobiliary calcium fluxes are attenuated in the perfused liver of rats made cholestatic with ethynylestradiol *in vivo* and with phalloidin *in vitro*," *Hepatology* 21:1455-1464, 1995).

An experiment with male and female rats (X. Mayol, "Ethinyl estradiol-induced cell proliferation in rat liver. Involvement of specific populations of hepatocytes," *Carcinogenesis* 13:2381-2388, 1992) found that 17α-ethinylestradiol induced acute liver hyperplasia (increase in mitotic index and BrdU staining) after two days of treatment, although growth regression occurred within the first few days of treatment. With long-term treatment, lasting hyperplasia was again observed after three to six months of administration of the drug. Apoptosis increased around day 3 and returned to normal by one week. Additional experiments in this same study showed that proliferating hepatocytes were predominantly located around a periportal zone of vacuolated hepatocytes, which were also induced by the treatment. Chronic induced activation was characterized by flow cytometry on hepatocytes isolated from male rats, and ploidy analysis of hepatocyte cell suspensions showed a considerably increased proportion of diploid hepatocytes. These diploid cells were the most susceptible to drug-induced proliferation. The results from this study support the theory that cell target populations exist that respond to the effects of tumor promoters. The susceptibility of the diploid hepatocytes to proliferation during treatment may explain, at least in part, the behavior of 17α-ethinylestradiol as a tumor promoter in the liver.

Wy-14643, a tumor-inducing compound that acts in the liver, has been used to study the genetic profile of cells during the various stages of carcinogenic development,

with a view toward developing strategies for detecting, diagnosing and treating cancers (J.C. Rockett *et al.*, "Use of suppression-PCR subtractive hybridisation to identify genes that demonstrate altered expression in male rat and guinea pig livers following exposure to Wy-14,643, a peroxisome proliferator and non-genotoxic hepatocarcinogen," *Toxicology* 144(1-3):13-29, 2000). In contrast to other carcinogens, Wy-14643 does not mutate DNA directly. Instead, it acts on the peroxisome proliferator activated receptor-alpha (PPARalpha), as well as on other signaling pathways that regulate growth (T.E. Johnson *et al.*, "Peroxisome proliferators and fatty acids negatively regulate liver X receptor-mediated activity and sterol biosynthesis," *J Steroid Biochem Mol Biol.* 77(1):59-71, 2001). The effect is elevated and sustained cell replication, accompanied by a decrease in apoptosis (I. Rusyn *et al.*, "Expression of base excision repair enzymes in rat and mouse liver is induced by peroxisome proliferators and is dependent upon carcinogenic potency," *Carcinogenesis* 21(12):2141-2145, 2000). These authors (Rusyn *et al.*) noted an increase in the expression of enzymes that repair DNA by base excision, but no increased expression of enzymes that do not repair oxidative damage to DNA. In a study on rodents, Johnson *et al.* noted that Wy-14643 inhibited liver-X-receptor-mediated transcription in a dose-dependent manner, as well as *de novo* sterol synthesis.

In experiments with mouse liver cells (J.M. Peters *et al.*, "Role of peroxisome proliferator-activated receptor alpha in altered cell cycle regulation in mouse liver," *Carcinogenesis* 19(11):1989-1994, 1998), exposure to Wy-14643 produced increased levels of acyl CoA oxidase and proteins involved in cell proliferation: CDK-1, 2 and 4, PCNA and c-myc. Elevated levels may be caused by accelerated transcription that is mediated directly or indirectly by PPARalpha. It is likely that the carcinogenic properties of peroxisome proliferators are due to the PPARalpha-dependent changes in levels of cell cycle regulatory proteins.

Another study on rodents (B.J. Keller *et al.*, "Several nongenotoxic carcinogens uncouple mitochondrial oxidative phosphorylation," Biochim Biophys Acta 1102(2):237-244, 1992) showed that Wy-14643 was capable of uncoupling oxidative phosphorylation in rat liver mitochondria. Rates of urea synthesis from ammonia and bile flow, two energy-dependent processes, were reduced, indicating that the energy supply for these processes was disrupted as a result of cellular exposure to the toxin.

Wy-14643 has also been shown to activate nuclear factor kappaB, NADPH oxidase and superoxide production in Kupffer cells (I. Rusyn *et al.*, "Oxidants from nicotinamide adenine dinucleotide phosphate oxidase are involved in triggering cell proliferation in the liver due to peroxisome proliferators," *Cancer Res* 60(17):4798-4803, 2000). NADPH oxidase is known to induce mitogens, which cause proliferation of liver cells.

CPA is a potent androgen antagonist and has been used to treat acne, male pattern baldness, precocious puberty, and prostatic hyperplasia and carcinoma (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 1453, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). Additionally, CPA has been used clinically in hormone replacement therapy (HRT). CPA is useful in HRT as it protects the endometrium, decreases menopausal symptoms, and lessens osteoporotic fracture risk (H.P. Schneider, "The role of antiandrogens in hormone replacement therapy," *Climacteric* 3 (Suppl. 2): 21-27, 2000).

Although CPA has numerous clinical applications, it is tumorigenic, mitogenic, and mutagenic. CPA has been used to treat patients with adenocarcinoma of the prostate, however in two documented cases (A.G. Macdonald and J.D. Bissett, "Avascular necrosis of the femoral head in patients with prostate cancer treated with cyproterone acetate and radiotherapy," *Clin Oncol* 13: 135-137, 2001), patients developed femoral head avascular necrosis following CPA treatment. In one study (O. Krebs *et al.*, "The DNA damaging drug cyproterone acetate causes gene mutations and induces glutathione-S-transferase P in the liver of female Big Blue transgenic F344 rats," *Carcinogenesis* 19(2): 241-245, 1998), Big Blue transgenic F344 rats were giving varying doses of CPA. As the dose of CPA increased, so did the mutation frequency, but a threshold dose was not determined. Another study (S. Werner *et al.*, "Formation of DNA adducts by cyproterone acetate and some structural analogues in primary cultures of human hepatocytes," *Mutat Res* 395(2-3): 179-187, 1997), showed that CPA caused the formation of DNA adducts in primary cultures of human hepatocytes. The authors suggest that the genotoxicity associated with CPA may be due to the double bond in position 6-7 of the steroid.

In additional experiments with rats (P. Kasper and L. Mueller, "Time-related induction of DNA repair synthesis in rat hepatocytes following *in vivo* treatment with cyproterone acetate," *Carcinogenesis* 17(10): 2271-2274, 1996), CPA was shown to induce unscheduled DNA synthesis *in vitro*. After a single oral dose of 100 mg CPA/kg

body weight, continuous DNA repair activity was observed after 16 hours. Furthermore, CPA increased the occurrence of S phase cells, which corroborated the mitogenic potential of CPA in rat liver.

CPA has also been shown to produce cirrhosis (B.Z. Garty *et al.*, "Cirrhosis in a child with hypothalamic syndrome and central precocious puberty treated with cyproterone acetate," *Eur J Pediatr* 158(5): 367-370, 1999). A child, who had been treated with CPA for over 4 years for hypothalamic syndrome and precocious puberty, developed cirrhosis. Even though the medication was discontinued, the child eventually succumbed to sepsis and multiorgan failure four years later.

In one study on rat liver treated with CPA (W. Bursch *et al.*, "Expression of clusterin (testosterone-repressed prostate message-2) mRNA during growth and regeneration of rat liver," *Arch Toxicol* 69(4): 253-258, 1995), the expression of clusterin, a marker for apoptosis, was examined and measured by Northern and slot blot analysis. Bursch *et al.* showed that post-CPA administration, the clusterin mRNA concentration level increased. Moreover, in situ hybridization demonstrated that clusterin was expressed in all hepatocytes, therefore it is not limited to cells in the process of death by apoptosis.

Diclofenac, a non-steroidal anti-inflammatory drug, has been frequently administered to patients suffering from rheumatoid arthritis, osteoarthritis, and ankylosing spondylitis. Following oral administration, diclofenac is rapidly absorbed and then metabolized in the liver by cytochrome P450 isozyme of the CYC2C subfamily (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 637, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). In addition, diclofenac has been applied topically to treat pain due to corneal damage (D.G. Jayamanne *et al.*, "The effectiveness of topical diclofenac in relieving discomfort following traumatic corneal abrasions," *Eye* 11(Pt. 1): 79-83, 1997; D.I. Dornic *et al.*, "Topical diclofenac sodium in the management of anesthetic abuse keratopathy," *Am J. Ophthalmol* 125(5): 719-721, 1998).

Although diclofenac has numerous clinical applications, adverse side-effects have been associated with the drug. In one study, out of 16 patients suffering from corneal complications associated with diclofenac use, 6 experienced corneal or scleral melts, three experienced ulceration, and two experienced severe keratopathy (A.C. Guidera *et al.*, "Keratitis, ulceration, and perforation associated with topical nonsteroidal anti-inflammatory drugs," *Ophthalmology* 108(5): 936-944, 2001). Another report described a

term newborn who had premature closure of the ductus arteriosus as a result of maternal treatment with diclofenac (M. Zenker *et al.*, "Severe pulmonary hypertension in a neonate caused by premature closure of the ductus arteriosus following maternal treatment with diclofenac: a case report," *J Perinat Med* 26(3): 231-234, 1998). Although it was only two weeks prior to delivery, the newborn had severe pulmonary hypertension and required treatment for 22 days of high doses of inhaled nitric oxide.

Another study investigated 180 cases of patients who had reported adverse reactions to diclofenac to the Food and Drug Administration (A.T. Banks *et al.*, "Diclofenac-associated hepatoxicity: analysis of 180 cases reported to the Food and Drug Administration as adverse reactions," *Hepatology* 22(3): 820-827, 1995). Of the 180 reported cases, the most common symptom was jaundice (75% of the symptomatic patients). Liver sections were taken and analyzed, and hepatic injury was apparent one month after drug treatment. An additional report showed that a patient developed severe hepatitis five weeks after beginning diclofenac treatment for osteoarthritis (A. Bhogaraju *et al.*, "Diclofenac-associated hepatitis," *South Med J* 92(7): 711-713, 1999). Within a few months following the cessation of diclofenac treatment there was complete restoration of liver functions.

In one study on diclofenac-treated Wistar rats (P.E. Ebong *et al.*, "Effects of aspirin (acetylsalicylic acid) and Cataflam (potassium diclofenac) on some biochemical parameters in rats," *Afr J Med Med Sci* 27(3-4): 243-246, 1998), diclofenac treatment induced an increase in serum chemistry levels of alanine aminotransferase, aspartate aminotransferase, methaemoglobin, and total and conjugated bilirubin. Additionally, diclofenac enhanced the activity of alkaline phosphatase and 5'nucleotidase. Another study showed that humans given diclofenac had elevated levels of hepatic transaminases and serum creatine when compared to the control group (F. McKenna *et al.*, "Celecoxib versus diclofenac in the management of osteoarthritis of the knee," *Scand J Rheumatol* 30(1): 11-18,, 2001).

Toxicity Prediction and Modeling

The genes and gene expression information, as well as the portfolios and subsets of the genes provided in Tables 1-3, may be used to predict at least one toxic effect, including the hepatotoxicity of a test or unknown compound. As used, herein, at least one toxic

effect includes, but is not limited to, a detrimental change in the physiological status of a cell or organism. The response may be, but is not required to be, associated with a particular pathology, such as tissue necrosis. Accordingly, the toxic effect includes effects at the molecular and cellular level. Hepatotoxicity is an effect as used herein and includes but is not limited to the pathologies of liver necrosis, hepatitis, fatty liver and protein adduct formation.

In general, assays to predict the toxicity or hepatotoxicity of a test agent (or compound or multi-component composition) comprise the steps of exposing a cell population to the test compound, assaying or measuring the level of relative or absolute gene expression of one or more of the genes in Tables 1-3 and comparing the identified expression level(s) to the expression levels disclosed in the Tables and database(s) disclosed herein. Assays may include the measurement of the expression levels of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100 or more genes from Tables 1-3.

In the methods of the invention, the gene expression level for a gene or genes induced by the test agent, compound or compositions may be comparable to the levels found in the Tables or databases disclosed herein if the expression level varies within a factor of about 2, about 1.5 or about 1.0 fold. In some cases, the expression levels are comparable if the agent induces a change in the expression of a gene in the same direction (*e.g.*, up or down) as a reference toxin.

The cell population that is exposed to the test agent, compound or composition may be exposed *in vitro* or *in vivo*. For instance, cultured or freshly isolated hepatocytes, in particular rat hepatocytes, may be exposed to the agent under standard laboratory and cell culture conditions. In another assay format, *in vivo* exposure may be accomplished by administration of the agent to a living animal, for instance a laboratory rat.

Procedures for designing and conducting toxicity tests in *in vitro* and *in vivo* systems are well known, and are described in many texts on the subject, such as *Loomis et al.* Loomis's Esstentials of Toxicology, 4th Ed. (Academic Press, New York, 1996); Echobichon, The Basics of Toxicity Testing (CRC Press, Boca Raton, 1992); Frazier, editor, *In Vitro* Toxicity Testing (Marcel Dekker, New York, 1992); and the like.

In *in vitro* toxicity testing, two groups of test organisms are usually employed: One group serves as a control and the other group receives the test compound in a single dose (for acute toxicity tests) or a regimen of doses (for prolonged or chronic toxicity

tests). Since in some cases, the extraction of tissue as called for in the methods of the invention requires sacrificing the test animal, both the control group and the group receiving compound must be large enough to permit removal of animals for sampling tissues, if it is desired to observe the dynamics of gene expression through the duration of an experiment.

In setting up a toxicity study, extensive guidance is provided in the literature for selecting the appropriate test organism for the compound being tested, route of administration. dose ranges, and the like. Water or physiological saline (0.9% NaCl in water) is the solute of choice for the test compound since these solvents permit administration by a variety of routes. When this is not possible because of solubility limitations, vegetable oils such as corn oil or organic solvents such as propylene glycol may be used.

Regardless of the route of administration, the volume required to administer a given dose is limited by the size of the animal that is used. It is desirable to keep the volume of each dose uniform within and between groups of animals. When rats or mice are used, the volume administered by the oral route generally should not exceed 0.005 ml per gram of animal. Even when aqueous or physiological saline solutions are used for parenteral injection the volumes that are tolerated are limited, although such solutions are ordinarily thought of as being innocuous. The intravenous LD_{50} of distilled water in the mouse is approximately 0.044 ml per gram and that of isotonic saline is 0.068 ml per gram of mouse. In some instances, the route of administration to the test animal should be the same as, or as similar as possible to, the route of administration of the compound to man for therapeutic purposes.

When a compound is to be administered by inhalation, special techniques for generating test atmospheres are necessary. The methods usually involve aerosolization or nebulization of fluids containing the compound. If the agent to be tested is a fluid that has an appreciable vapor pressure, it may be administered by passing air through the solution under controlled temperature conditions. Under these conditions, dose is estimated from the volume of air inhaled per unit time, the temperature of the solution, and the vapor pressure of the agent involved. Gases are metered from reservoirs. When particles of a solution are to be administered, unless the particle size is less than about 2 μm the particles will not reach the terminal alveolar sacs in the lungs. A variety of apparatuses and

chambers are available to perform studies for detecting effects of irritant or other toxic endpoints when they are administered by inhalation. The preferred method of administering an agent to animals is via the oral route, either by intubation or by incorporating the agent in the feed.

When the agent is exposed to cells *in vitro* or in cell culture, the cell population to be exposed to the agent may be divided into two or more subpopulations, for instance, by dividing the population into two or more identical aliquots. In some prefered embodiments of the methods of the invention, the cells to be exposed to the agent are derived from liver tissue. For instance, cultured or freshly isolated rat hepatocytes may be used.

The methods of the invention may be used to generally predict at least one toxic response, and as described in the Examples, may be used to predict the likelihood that a compound or test agent will induce various specifc liver pathologies such as liver necrosis, fatty liver disease, protein adduct formation or hepatitis. The methods of the invention may also be used to determine the similarity of a toxic response to one or more individual compounds. In addition, the methods of the invention may be used to predict or elucidate the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin (see Tables 3A-3S).

Diagnostic Uses for the Toxicity Markers

As described above, the genes and gene expression information or portfolios of the genes with their expression information as provided in Tables 1-3 may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or to identify or predict the toxic effects of a compound or agent. For instance, a tissue sample such as a sample of peripheral blood cells or some other easily obtainable tissue sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-3 may be compared to the expression levels found in tissues or cells exposed to the toxins described herein. These methods may result in the diagnosis of a physiological state in the cell or may be used to identify the potential toxicity of a compound, for instance a new or unknown compound or agent. The comparison of expression data, as well as available

sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described below.

In another format, the levels of a gene(s) of Tables 1-3, its encoded protein(s), or any metabolite produced by the encoded protein may be monitored or detected in a sample, such as a bodily tissue or fluid sample to identify or diagnose a physiological state of an organism. Such samples may include any tissue or fluid sample, including urine, blood and easily obtainable cells such as peripheral lymphocytes.

Use of the Markers for Monitoring Toxicity Progression

As described above, the genes and gene expression information provided in Tables 1-3 may also be used as markers for the monitoring of toxicity progression, such as that found after initial exposure to a drug, drug candidate, toxin, pollutant, etc. For instance, a tissue or cell sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-3 may be compared to the expression levels found in tissue or cells exposed to the hepatotoxins described herein. The comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases.

Use of the Toxicity Markers for Drug Screening

According to the present invention, the genes identified in Tables 1-3 may be used as markers or drug targets to evaluate the effects of a candidate drug, chemical compound or other agent on a cell or tissue sample. The genes may also be used as drug targets to screen for agents that modulate their expression and/or activity. In various formats, a candidate drug or agent can be screened for the ability to simulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers which the drug induces and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

Assays to monitor the expression of a marker or markers as defined in Tables 1-3

may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to one, tow or more genes from Tables 1-3 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell. Cell lines, tissues or other samples are first exposed to a test agent and in some instances, a known toxin, and the detected expression levels of one or more, or preferably 2 or more of the genes of Tables 1-3 are compared to the expression levels of those same genes exposed to a known toxin alone. Compounds that modulate the expression patterns of the known toxin(s) would be expected to modulate potential toxic physiological effects *in vivo*. The genes in Tables 1-3 are particularly appropriate marks in these assays as they are differentially expressed in cells upon exposure to a known hepatotoxin.

In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the transcriptional regulatory regions of a gene in Tables 1-3 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990) Anal. Biochem. 188:245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 1-3. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory Press, 1989).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would

be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the gene products of Tables 1-3 fused to one or more antigenic fragments or other detectable markers, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct or other detectable tag. Such a process is well known in the art (see Maniatis).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample is then compared with the control samples (no exposure and exposure to a known toxin) where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control is used to distinguish the effectiveness and/or toxic effects of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-3. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein (Tables 1-3) between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population and a cell population exposed to a known toxin may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant GA. in: Meyers (ed.) Molecular Biology and Biotechnology (New York, VCH Publishers, 1995), pp. 659-664). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Nucleic Acid Assay Formats

The genes identified as being differentially expressed upon exposure to a known hepatotoxin (Tables 1-3) may be used in a variety of nucleic acid detection assays to detect or quantititate the expression level of a gene or multiple genes in a given sample. The genes described in Tables 1-3 may also be used in combination with one or more additional genes whose differential expression is associate with toxicity in a cell or tissue. In preferred embodiments, the genes in Tables 1-3 may be combined with one or more of the genes described in related applications 60/222,040, 60/244,880, 60/290,029, 60/290,645, 60/292,336, 60/295,798, 60/297,457, 60/298,884 and 60/303,459, all of which are incorporated by reference on page 1 of this application.

Any assay format to detect gene expression may be used. For example, traditional Northern blotting, dot or slot blot, nuclease protection, primer directed amplification, RT-PCR, semi- or quantitative PCR, branched-chain DNA and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention. In cases where smaller numbers of genes are detected, amplification based assays may be most efficient. Methods and assays of the invention, however, may be most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, particles, beads, microparticles or silicon or glass based chips, etc. Such chips, wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755).

Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be

on the order of about a square centimeter. Probes corresponding to the genes of Tables 1-3 or from the related applications described above may be attached to single or multiple solid support structures, *e.g.*, the probes may be attached to a single chip or to multiple chips to comprise a chip set.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart et al., Nat. Biotechnol. (1996) 14, 1675-1680; McGall *et al., Proc. Nat. Acad. Sci.* USA (1996) 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 1-3. For instance, such arrays may contain oligonucleotides that are complementary or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more the genes described herein. Preferred arrays contain all or nearly all of the genes listed in Tables 1-3, or individually, the gene sets of Tables 3A-3S. In a preferred embodiment, arrays are constructed that contain oligonucleotides to detect all or nearly all of the genes in any one of or all of Tables 1-3 on a single solid support substrate, such as a chip.

The sequences of the expression marker genes of Tables 1-3 are in the public databases. Table 1 provides the GenBank Accession Number for each of the sequences (see *www.ncbi.nlm.nih.gov/*). The sequences of the genes in GenBank are expressly herein incorporated by reference in their entirety as of the filing date of this application, as are related sequences, for instance, sequences from the same gene of different lengths, variant sequences, polymorphic sequences, genomic sequences of the genes and related sequences from different species, including the human counterparts, where appropriate. These sequences may be used in the methods of the invention or may be used to produce the probes and arrays of the invention. In some embodiments, the genes in Tables 1-3 that correspond to the genes or fragments previously associated with a toxic response may be excluded from the Tables.

As described above, in addition to the sequences of the GenBank Accessions Numbers disclosed in the Tables 1-3 , sequences such as naturally occurring variant or polymorphic sequences may be used in the methods and compositions of the invention. For instance, expression levels of various allelic or homologous forms of a gene disclosed in the Tables 1-3 may be assayed. Any and all nucleotide variations that do not alter the functional activity of a gene listed in the Tables 1-3 , including all naturally occurring

allelic variants of the genes herein disclosed, may be used in the methods and to make the compositions (*e.g.*, arrays) of the invention.

Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for screening or assaying a tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-3 refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average

hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.* probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 different nucleic acid hybridizations.

As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

The terms "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na^+ ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (*e.g.* nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Probe design

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of test probes that specifically hybridize to the sequences of interest. Probes may be produced from any region of the genes identified in the Tables and the attached representative sequence listing. In instances where the gene reference in the Tables is an EST, probes may be designed from that sequence or from other regions of the corresponding full-length transcript that may be available in any of the sequence databases, such as those herein described. See WO99/32660 for methods of producing probes for a given gene or genes. In addition, any available software may be used to produce specific probe sequences, including, for instance, software available from Molecular Biology Insights, Olympus Optical Co. and Biosoft International. In a preferred embodiment, the array will also include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500, or about 7 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 35 nucleotides in length. In other particularly preferred embodiments, the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes may fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*,

fluorescence intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent) Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is

directed. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation, for instance, a mutation of a gene in the accompanying Tables 1-3 . The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

Cell or tissue samples may be exposed to the test agent *in vitro* or *in vivo*. When cultured cells or tissues are used, appropriate mammalian liver extracts may also be added with the test agent to evaluate agents that may require biotransformation to exhibit toxicity. In a preferred format, primary isolates of animal or human hepatocytes which already express the appropriate complement of drug-metabolizing enzymes may be exposed to the test agent without the addition of mammalian liver extracts.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not. The genes may be amplified or not. The cloning and/or amplification do not appear to bias the representation of genes within a population. In some assays, it may be preferable, however, to use polyA+ RNA as a source, as it can be used with less processing steps.

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation, P. Tijssen, Ed., Elsevier, N.Y. (1993). Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates are used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells.

Frequently the sample will be a tissue or cell sample that has been exposed to a compound, agent, drug, pharmaceutical composition, potential environmental pollutant or other composition. In some formats, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Forming High Density Arrays

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling. See Pirrung, U.S. Patent No. 5,143,854.

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO93/09668 and WO01/23614. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or

natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

In a preferred embodiment, hybridization is performed at low stringency, in this case in 6X SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, I X SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25 X SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the

hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO99/32660.

Databases

The present invention includes relational databases containing sequence information, for instance, for the genes of Tables 1-3, as well as gene expression information from tissue or cells exposed to various standard toxins, such as those herein described (see Table 3A-3S). Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information (see Table 1), or descriptive information concerning the clinical status of the tissue sample, or the animal from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases are widely available, for instance, see U.S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

The databases of the invention may be linked to an outside or external database such as GenBank (*www.ncbi.nlm.nih.gov/entrez.index.html*); KEGG (*www.genome.ad.jp/kegg*); SPAD (*www.grt.kyushu-u.ac.jp/spad/index.html*); HUGO (*www.gene.ucl.ac.uk/hugo*); Swiss-Prot (*www.expasy.ch.sprot*); Prosite (*www.expasy.ch/tools/scnpsit1.html*); OMIM (*www.ncbi.nlm.nih.gov/omim*); GDB (*www.gdb.org*); and GeneCard (*bioinformatics.weizmann.ac.il/cards*). In a preferred embodiment, as described in Tables 1-3, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI) (*www.ncbi.nlm.nih.gov*).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or information provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such has those available from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising one or more of the genes in Tables 1-3, comprising the step of comparing the expression level of at least one gene in Tables 1-3 in a cell or tissue exposed to a test agent to the level of expression of the gene in the database. Such methods may be used to predict the toxic potential of a given compound by comparing the level of expression of a gene or genes in Tables 1-3 from a tissue or cell sample exposed to the test agent to the expression levels found in a control tissue or cell samples exposed to a standard toxin or hepatotoxin such as those herein described. Such methods may also be used in the drug or agent screening assays as described below.

Kits

The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, protein reagents encoded by the genes of the Tables, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to predict or model the toxic response of a test compound, to monitor the progression of hepatic disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

The databases packaged with the kits are a compilation of expression patterns from

human or laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-3). In particular, the database software and packaged information include the expression results of Tables 1-3 that can be used to predict toxicity of a test agent by comparing the expression levels of the genes of Tables 1-3 induced by the test agent to the expression levels presented in Tables 3A-3S. In another format, database and software information may be provided in a remote electronic format, such as a website, the address of which may be packaged in the kit.

The kits may used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

Databases and software designed for use with use with microarrays is discussed in Balaban *et al.*, U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed Tables 1-3 , collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Identification of Toxicity Markers

The hepatotoxins amitryptiline, ANIT, acetaminophen, carbon tetrachloride, CPA, diclofenac, estradiol, indomethacin, valproate, WY-14643 and control compositions were administered to male Sprague-Dawley rats at various time points using adminstration diluents, protocols and dosing regimes as previously described in the art and previously described in the priority applications discussed above.

After adminstration, the dosed animals were observed and tissues were collected as described below:

OBSERVATION OF ANIMALS

1. Clinical Observations — Twice daily - mortality and moribundity check. Cage Side Observations - skin and fur, eyes and mucous membrane, respiratory system, circulatory system, autonomic and central nervous system, somatomotor pattern, and behavior pattern. Potential signs of toxicity, including tremors, convulsions, salivation, diarrhea, lethargy, coma or other atypical behavior or appearance, were recorded as they occurred and included a time of onset, degree, and duration.

2. Physical Examinations — Prior to randomization, prior to initial treatment, and prior to sacrifice.

3. Body Weights — Prior to randomization, prior to initial treatment, and prior to sacrifice.

CLINICAL PATHOLOGY

1. Frequency — Prior to necropsy.

2. Number of animals	All surviving animals.
3. Bleeding Procedure	Blood was obtained by puncture of the orbital sinus while under 70% CO_2/ 30% O_2 anesthesia.
4. Collection of Blood Samples	Approximately 0.5 mL of blood was collected into EDTA tubes for evaluation of hematology parameters.
	Approximately 1 mL of blood was collected into serum separator tubes for clinical chemistry analysis.
	Approximately 200 uL of plasma was obtained and frozen at ~-80°C for test compound/metabolite estimation.
	An additional ~2 mL of blood was collected into a 15 mL conical polypropylene vial to which ~3 mL of Trizol was immediately added. The contents were immediately mixed with a vortex and by repeated inversion. The tubes were frozen in liquid nitrogen and stored at ~-80°C.

TERMINATION PROCEDURES

Terminal Sacrifice

Approximately 1 and 3 and 6 and 24 and 48 hours and 5-7 days after the initial dose, rats were weighed, physically examined, sacrificed by decapitation, and exsanguinated. The animals were necropsied within approximately five minutes of sacrifice. Separate sterile, disposable instruments were used for each animal, with the exception of bone cutters, which were used to open the skull cap. The bone cutters were dipped in disinfectant solution between animals.

Necropsies were conducted on each animal following procedures approved by board-certified pathologists.

Animals not surviving until terminal sacrifice were discarded without necropsy (following euthanasia by carbon dioxide asphyxiation, if moribund). The approximate time of death for moribund or found dead animals was recorded.

Postmortem Procedures

Fresh and sterile disposable instruments were used to collect tissues. Gloves were worn at all times when handling tissues or vials. All tissues were collected and frozen within approximately 5 minutes of the animal's death. The liver sections and kidneys were frozen within approximately 3-5 minutes of the animal's death. The time of euthanasia, an interim time point at freezing of liver sections and kidneys, and time at completion of necropsy were recorded. Tissues were stored at approximately -80°C or preserved in 10% neutral buffered formalin.

Tissue Collection and Processing

Liver

1. Right medial lobe – snap frozen in liquid nitrogen and stored at ~-80°C.
2. Left medial lobe - Preserved in 10% neutral-buffered formalin (NBF) and evaluated for gross and microscopic pathology.
3. Left lateral lobe – snap frozen in liquid nitrogen and stored at ~-80°C.

Heart

A sagittal cross-section containing portions of the two atria and of the two ventricles was preserved in 10% NBF. The remaining heart was frozen in liquid nitrogen and stored at ~-80°C.

3. Kidneys (both)

1. Left – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at ~ -80°C.
2. Right – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at ~ -80°C.

4. Testes (both)
A sagittal cross-section of each testis was preserved in 10% NBF. The remaining testes were frozen together in liquid nitrogen and stored at ~ -80°C.

Brain (whole)

1. A cross-section of the cerebral hemispheres and of the diencephalon was preserved in 10% NBF, and the rest of the brain was frozen in liquid nitrogen and stored at ~ -80°C.

Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500 μg per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μg/ml. From 2 μg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript in vitro Transcription Kit.

To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol (Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Tris-acetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C. Following the Affymetrix protocol, 55 μg of fragmented cRNA was hybridized on the Affymetrix rat array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The

chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip□ version 3.0 and Expression Data Mining (EDMT) software (version 1.0), GeneExpress2000, and S-Plus.

Table 1 discloses those genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession and Sequence Identification numbers, the identities of the metabolic pathways in which the genes function, the gene names if known, and the unigene cluster titles. The comparison code represents the various toxicity or liver pathology state that each gene is able to discriminate as well as the individual toxin type associated with each gene. The codes are defined in Table 2. The GLGC ID is the internal Gene Logic identification number.

Table 2 defines the comparison codes used in Table 1.

Tables 3A-3S disclose the summary statistics for each of the comparisons performed. Each gene is identified by its Gene Logic identification number and can be cross-referenced to a gene name and representative SEQ ID NO. in Table 1. The group mean (*eg.* toxicity group) is the mean signal intensity as normalized for the various chip parameters in the samples that are being assayed for in the particular comparison. The non-group (*eg.* non-toxicity group) mean represents the mean signal intensity as normalized for the various chip parameters in the samples that are not being assayed for in the particular comparison. The mean values are derived from Average Difference (AveDiff) values for a particular gene, averaged across the corresponding samples. Each individual Average Difference value is calculated by integrating the intensity information from multiple probe pairs that are tiled for a particular fragment. The normalization algorithm used to calculate the AveDiff is based on the observation that the expression intensity values from a single chip experiment have different distributions, depending on whether small or large expression values are considered. Small values, which are assumed to be mostly noise, are approximately normally distributed with mean zero, while larger values roughly obey a log-normal distribution; that is, their logarithms are normally distributed with some nonzero mean.

The normalization process computes separate scale factors for "non-expressors" (small values) and "expressors" (large ones). The inputs to the algorithm are pre-normalized Average Difference values, which are already scaled to set the trimmed mean equal to 100. The algorithm computes the standard deviation SD noise of the negative values, which are assumed to come from non-expressors. It then multiplies all negative values, as well as all positive values less than 2.0* SD noise, by a scale factor proportional to 1/ SD noise.

Values greater than 2.0* SD noise are assumed to come from expressors. For these values, the standard deviation SD log (signal) of the logarithms is calculated. The logarithms are then multiplied by a scale factor proportional to 1/ SD log (signal) and exponentiated . The resulting values are then multiplied by another scale factor, chosen so there will be no discontinuity in the normalized values from unscaled values on either side of 2.0* SD noise. Some AveDiff values may be negative due to the general noise involved in nucleic acid hybridization experiments. Although many conclusions can be made corresponding to a negative value on the GeneChip platform, it is difficult to assess the meaning behind the negative value for individual fragments. Our observations show that, although negative values are observed at times within the predictive gene set, these values reflect a real biological phenomenon that is highly reproducible across all the samples from which the measurement was taken. For this reason, those genes that exhibit a negative value are included in the predictive set. It should be noted that other platforms of gene expression measurement may be able to resolve the negative numbers for the corresponding genes. The predictive ability of each of those genes should extend across platforms, however. Each mean value is accompanied by the standard deviation for the mean. LDA is the linear discriminant analysis that measures the ability of each gene to predict whether or not a sample is toxic. The LDA score is calculated by the following steps:

Calculation of a discriminant score.

Let X_i represent the AveDiff values for a given gene across the Group 1 samples, i=1...n.

Let Y_i represent the AveDiff values for a given gene across the Group 2 samples, i=1...t.

The calculations proceed as follows:

1. Calculate mean and standard deviation for X_i's and Y_i's, and denote these by m_X, m_Y, s_X,s_Y.
2. For all X_i's and Y_i's, evaluate the function $f(z) = ((1/s_Y)*\exp(-.5*((z-m_Y)/s_Y)^2)) / (((1/s_Y)*\exp(-.5*((z-m_Y)/s_Y)^2)) +((1/s_X)*\exp(-.5*((z-m_X)/s_X)^2)))$.
3. The number of correct predictions, say P, is then the number of Y_i's such that $f(Y_i)>.5$ plus the number of X_i's such that $f(X_i)<.5$.
4. The discriminant score is then P/(n+t)

Linear discriminant analysis uses both the individual measurements of each gene and the calculated measurements of all combinations of genes to classify samples. For each gene a weight is derived from the mean and standard deviation of the tox and nontox groups. Every gene is multiplied by a weight and the sum of these values results in a collective discriminate score. This discriminant score is then compared against collective centroids of the tox and nontox groups. These centroids are the average of all tox and nontox samples respectively. Therefore, each gene contributes to the overall prediction. This contribution is dependent on weights that are large positive or negative numbers if the relative distances between the tox and nontox samples for that gene are large and small numbers if the relative distances are small. The discriminant score for each unknown sample and centroid values can be used to calculate a probability between zero and one as to which group the unknown sample belongs.

Example 2: General Toxicity Modeling

Samples were selected for grouping into tox-responding and non-tox-responding groups by examining each study individually with PCA to determine which treatments had an observable response. Only groups where confidence of their tox-responding and non-tox-responding status was established were included in building a general tox model.

Two general types of models were built for general toxicity determination. One model used information from the expression patterns of each gene individually and then combined all the information using linear weights for each gene. The second type determined orthogonal vectors describing all the expression information collectively and used these composite vectors to predict toxicity.

Over 500 linear discriminant models were generated to describe toxic and non-toxic samples. The top 10, 25, 50 and 100 discriminant genes were used to determine

toxicity by calculating each gene's contribution with homo and heteroscedastic treatment of variance and inclusion or exclusion of mutual information between genes. Prediction of samples within the database exceeded 90% for most models. In addition, models were built by sequential use of two, five, ten, twenty five, and fifty genes, starting with the best discriminators and proceeding to the worst discriminators without replication. All discriminating genes and/or ESTs had at least 70% discriminate ability, which was previously determined to be significant via randomization experiments. It was determined that combinations of genes generally provided a better predictive ability then individual genes and that the more genes used the better predictive ability. It was also determined that combining the worst fifty discriminating genes provided better prediction than the best single gene and that many combinations of two or more genes provided better prediction than the best individual gene. Although the preferred embodiment includes fifty or more genes, many pairings or greater combinations of genes can work better than individual genes. All combinations of two or more genes from the selected list may be used to predict toxicity. These combinations could be selected by pairing in an ordered, agglomerate, divisive, or random approach. Further, as yet undetermined genes could be combined with individual or combination of genes described here to increase predictive ability. However, the genes described here may contribute most of the predictive ability of any such undetermined combinations.

The second approach used has been described in U.S. Provisional Application 60/_____ , using this approach all 527 genes and/or EST were used to predict toxic from non-toxic samples with greater than 94% accuracy when 15 components are used. Although using the first fifteen components provided a preferred model, other variations of this method can provide adequate predictive ability. These include selective inclusion of components via agglomerate, divisive, or random approaches or extraction of loading and combining them in ordered, agglomerate, divisive, or random approaches. Also the use of these composite variables in logistic regression to determine classification of samples can also be accomplished with linear discriminate analysis, neural or Bayesian networks, or other forms of regression and classification based on categorical or continual dependent and independent variables.

Example 3: Modeling Methods

The above modeling methods provide broad approaches of combining the expression of genes to predict sample toxicity. One method uses each variable individually and weights them; the other combines variables as a composite measure and adds weights to them after combination into a new variable. One could also provide no weight in a simple voting method or determine weights in a supervised or unsupervised method using agglomerate, divisive, or random approaches. All or selected combinations of genes may be combined in ordered, agglomerate, or divisive, supervised or unsupervised clustering algorithms with unknown samples for classification. Any form of correlation matrix may also be used to classify unknown samples. The spread of the group distribution and discriminate score alone provide enough information to enable a skilled person to generate all of the above types of models with accuracy that can exceed discriminate ability of individual genes. Some examples of methods that could be used individually or in combination after transformation of data types include but are not limited to: Discriminant Analysis, Multiple Discriminant Analysis, logistic regression, multiple regression analysis, linear regression analysis, conjoint analysis, canonical correlation, hierarchical cluster analysis, k-means cluster analysis, self-organizing maps, multidimensional scaling, structural equation modeling, support vector machine determined boundaries, factor analysis, neural networks, bayesian classifications, and resampling methods.

Example 4: Grouping of Individual compound and Pathology Classes

Samples were grouped into individual pathology classes based on known toxicological responses and observed clinical chemical and pathology measurements or into early and late phases of observable toxicity within a compound (Tables 3A-3S). The top 10, 25, 50, 100 genes based on individual discriminate scores were used in a model to ensure that combination of genes provided a better prediction than individual genes. As described above, all combinations of two or more genes from this list could potentially provide better prediction than individual genes when selected in any order or by ordered, agglomerate, divisive, or random approaches. In addition, combining these genes with other genes could provide better predictive ability, but most of this predictive ability would come from the genes listed here.

Samples may be considered toxic if they score positive in any pathological or individual compound class represented here or in any modeling method mentioned under general toxicology models based on combination of individual time and dose grouping of individual toxic compounds obtainable from the data. The pathological groupings and early and late phase models are preferred examples of all obtainable combinations of sample time and dose points. Most logical groupings with one or more genes and one or more sample dose and time points should produce better predictions of general toxicity, pathological specific toxicity, or similarity to known toxicant than individual genes.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

TABLE 1						Document Number 1650775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19	N	1729	NM_017258		B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
20	L,N	1729	NM_017258		B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
43	E,P	1698	NM_022287	Glycosaminoglycan degradation	HMm:alpha-L-iduronidase	Rattus norvegicus sulfate anion transporter (sat-1) mRNA, complete cds
55	O	1535	NM_012511	Oxidative phosphorylation	ATPase, Cu++ transporting, beta polypeptide (same as Wilson disease)	ATPase, Cu++ transporting, beta polypeptide (same as Wilson disease)
64	H	1620	NM_016991		Adrenergic, alpha 1B-, receptor	Adrenergic, alpha 1B-, receptor
72	F	1420	M57263		Hsp:PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K	Rat protein-glutamine gamma-glutamyltransferase mRNA, complete cds
90	E	1454	U20796			Rattus norvegicus nuclear receptor Rev-ErbA-beta mRNA, partial cds
134	A	1346	D87839	Alanine and aspartate metabolism, Butanoate metabolism, Glutamate metabolism, Propanoate metabolism, beta-Alanine metabolism	HHs:4-aminobutyrate aminotransferase	Rattus norvegicus mRNA for beta-alanine oxoglutarate aminotransferase, complete cds
135	A	1346	D87839	Alanine and aspartate metabolism,Butanoate metabolism,Glutamate metabolism,Propanoate metabolism,beta-Alanine metabolism	HHs:4-aminobutyrate aminotransferase	Rattus norvegicus mRNA for beta-alanine oxoglutarate aminotransferase, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
154	P,Q	1712	NM_022849		crp-ductin	Rattus norvegicus ebnerin mRNA, complete cds
155	P	1712	NM_022849		crp-ductin	Rattus norvegicus ebnerin mRNA, complete cds
164	H	538	AI010480	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism	Malate dehydrogenase 2, NAD (mitochondrial)	Rat mRNA for mitochondrial malate dehydrogenase (EC 1.1.1.37)
228	D	1452	U20194			Rattus norvegicus complement C8 beta (C8b) mRNA, partial cds
291	O	1538	NM_012522	Glycine, serine and threonine metabolism, Methionine metabolism, Selenoamino acid metabolism	Cystathionine beta synthase	Cystathionine beta synthase
330	R	1251	AI235460			Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
347	J	1443	U01914			Rattus norvegicus AKAP95 mRNA, partial cds
351	A	1720	NM_024127		HHs:growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds
352	A,J	1720	NM_024127		HHs:growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds
353	A,B,C,J	1720	NM_024127		HHs:growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds
354	A,J,Q	1720	NM_024127		HHs:growth arrest and DNA-damage-inducible, alpha	Rattus norvegicus GADD45 mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
355	N	1600	NM_013086		CAMP responsive element modulator,transcriptional repressor CREM	CAMP responsive element modulator
356	N	1658	NM_017334		CAMP responsive element modulator	CAMP responsive element modulator
360	R	1728	NM_012894		RNA editing deaminase of glutamate receptors	RNA editing deaminase of glutamate receptors
372	F,M	1482	U94708			Rattus norvegicus prostaglandin E receptor EP2 subtype mRNA, complete cds
373	P	1578	NM_012833		Canalicular multispecific organic anion transporter	Canalicular multispecific organic anion transporter
384	O	1457	U25137			Rattus norvegicus alternatively spliced signal transducer and regulator of transcription 5a2 (STAT5a2) mRNA, partial cds
396	M	1464	U49694		Hsp:CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE	Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds
397	S	1614	NM_013214		acyl-CoA hydrolase	Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds,acyl-CoA hydrolase
402	N	1734	NM_022403	Tryptophan metabolism	HHs:tryptophan 2,3-dioxygenase	Rat tryptophan-2,3-dioxygenase mRNA, complete cds
466	L	1517	X81395		Hsp:LIVER CARBOXYLESTERASE 3 PRECURSOR	R.norvegicus mRNA for pI 5.5 esterase (ES-3)

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
475	F	1224	AI233828			ESTs, Moderately similar to LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR [M.musculus]
488	F	1350	E00717	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
489	F	1540	NM_012540	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
494	G	1581	NM_012880		Superoxide dimutase 3	Superoxide dimutase 3
498	C	402	AA956278			ESTs
556	A,E	1575	NM_012803		Protein C	Protein C
563	M	1536	NM_012516		Complement component 4 binding protein, alpha	Complement component 4 binding protein, alpha
573	A	1169	AI232087			R.norvegicus mRNA for (S)-2-hydroxy acid oxidase
574	H,I	1682	NM_019905		calpactin I heavy chain	R.norvegicus mRNA for (S)-2-hydroxy acid oxidase,Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds,calpactin I heavy chain
633	A,G	1146	AI231127			ESTs
634	P	1381	K01932	Glutathione metabolism	Hsp:GLUTATHIONE S-TRANSFERASE YC-1	Rat liver glutathione S-transferase Yc subunit mRNA, complete cds
635	P	1515	X78848			Rat liver glutathione S-transferase Yc subunit mRNA, complete cds
650	J	1607	NM_013134	Sterol biosynthesis	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase

TABLE 1 Document Number 1650775

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
651	J	1607	NM_013134	Sterol biosynthesis	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
671	B	1445	U04808			Rattus norvegicus Sprague-Dawley putative G-protein coupled receptor (GCR) mRNA, complete cds
672	O	1492	X13722		Low density lipoprotein receptor	Rat mRNA for LDL-receptor
682	P	1627	NM_017051		Superoxide dimutase 2, mitochondrial	Superoxide dimutase 2, mitochondrial
699	M,P	1465	U55765			Rattus norvegicus RASP1 mRNA, complete cds
729	O	1429	M95762			Rattus norvegicus GABA transporter GAT-2 mRNA, complete cds
761	A	41	AA817685			Rattus norvegicus mRNA for cytochrome b5
794	A,D,E,G	1472	U68168	Tryptophan metabolism	HHs:kynureninase (L-kynurenine hydrolase)	Rattus norvegicus L-kynurenine hydrolase mRNA, complete cds
809	J	1451	U17035			Rattus norvegicus interferon inducible protein 10 (IP-10) mRNA, complete cds
811	A	1342	D63704	Pantothenate and CoA biosynthesis,Pyrimidine metabolism,beta-Alanine metabolism	HHs:dihydropyrimidinase	Rat mRNA for dihydropyrimidinase, complete cds
812	A	1342	D63704	Pantothenate and CoA biosynthesis,Pyrimidine metabolism,beta-Alanine metabolism	HHs:dihydropyrimidinase	EST, Highly similar to DPYS_RAT DIHYDROPYRIMIDINASE [R.norvegicus],Rat mRNA for dihydropyrimidinase, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
820	E	238	AA892395	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis,Pentose phosphate cycle	Aldolase B, fructose-biphosphate	Aldolase B, fructose-biphosphate
825	A	381	AA946108			Rattus norvegicus laminin-5 alpha 3 chain mRNA, complete cds
851	A	1721	NM_024132		fatty acid amide hydrolase	Rattus norvegicus fatty acid amide hydrolase mRNA, complete cds
906	K	1480	U83112			Rattus norvegicus INS-1 winged helix mRNA, complete cds
912	A	1467	U59184		Bcl2-associated X protein	Bcl2-associated X protein
923	A,J	1632	NM_017076		Tumor-associated glycoprotein pE4	Tumor-associated glycoprotein pE4
945	P	1349	D88666			Rattus norvegicus mRNA for PS-PLA1, complete cds
955	M	1471	U67138			Rattus norvegicus PSD-95/SAP90-associated protein-2 mRNA, complete cds
958	I,Q	1591	NM_012977		Lectin, galactose binding, soluble 9 (Galectin-9)	Lectin, galactose binding, soluble 9 (Galectin-9)
961	A	1573	NM_012796	Glutathione metabolism	Glutathione S-transferase 1 (theta)	Glutathione S-transferase 1 (theta)
1007	A	1589	NM_012942	Bile acid biosynthesis	Cytochrom P450 (cholesterol hydroxylase 7 alpha)	Cytochrom P450 (cholesterol hydroxylase 7 alpha)
1037	I	1500	X57523		Transporter 1, ABC (ATP binding cassette)	R.norvegicus mtp1 mRNA
1099	A	1678	NM_019303		Cytochrome P450, subfamily IIF, polypeptide 1	Cytochrome P450, subfamily IIF, polypeptide 1
1114	N	586	AI029917			Rattus norvegicus neuron-specific enolase (NSE) mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1126	A,I	1143	AI231007			Rattus norvegicus cca1 mRNA, complete cds
1141	E,Q	1505	X59601			Rat mRNA for plectin
1169	E,H	1008	AI177161			Rattus norvegicus NF-E2-related factor 2 mRNA, complete cds
1173	A	1661	NM_019184	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
1174	N	1661	NM_019184	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
1175	A,E,M	1661	NM_019184	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
1183	J	485	AF013144		Hsp:DUAL SPECIFICITY PROTEIN PHOSPHATASE 5	Rattus norvegicus MAP-kinase phosphatase (cpg21) mRNA, complete cds
1221	B,F,Q	1326	D11445			Rattus norvegicus mRNA for gro, complete cds
1223	E	1423	M75281			Rat cystatin S (CysS) gene, complete cds
1246	A	1569	NM_012770	Purine metabolism	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)
1258	I	1611	NM_013185		Hemopoietic cell tyrosine kinase	Hemopoietic cell tyrosine kinase
1271	Q	1384	L07073			Rat clathrin-associated adaptor protein homolog (p47A) mRNA, complete cds
1279	F	1477	U75916			Rattus norvegicus zonula occludens 2 protein (ZO-2) mRNA, partial cds
1305	J	1636	NM_017127	Glycerolipid metabolism	choline kinase	choline kinase
1306	J	1636	NM_017127	Glycerolipid metabolism	choline kinase	choline kinase
1394	G	1461	U37099			Rattus norvegicus GTP-binding protein (rab 3C) mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1399	C,D,G	1623	NM_017006	Glutathione metabolism, Pentose phosphate cycle	Glucose-6-phosphate dehydrogenase	Glucose-6-phosphate dehydrogenase
1409	A	560	AI012802	Pyruvate metabolism	HHs:hydroxyacyl glutathione hydrolase	Rattus norvegicus round spermatid protein RSP29 gene, complete cds
1411	C,D	920	AI172075			ESTs
1426	Q	1528	Z48225			R.norvegicus mRNA for protein synthesis initiation factor eIF-2B delta subunit
1430	M	1542	NM_012545	Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic L-amino acid decarboxylase)
1447	F	1651	NM_017281		proteasome (prosome, macropain) subunit, alpha type 4	proteasome (prosome, macropain) subunit, alpha type 4
1460	C,D	1439	S76054		Keratin 8	Keratin 8
1475	J	1386	L16764		Heat shock protein 70-1,S100 calcium binding protein A1	Rattus norvegicus S100A1 gene,Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
1478	A	1566	NM_012744	Alanine and aspartate metabolism,Citrate cycle (TCA cycle),Pyruvate metabolism	Pyruvate carboxylase	Pyruvate carboxylase
1479	A,G,K	1566	NM_012744	Alanine and aspartate metabolism,Citrate cycle (TCA cycle),Pyruvate metabolism	Pyruvate carboxylase	Pyruvate carboxylase
1501	A,C,F,H	690	AI072634			Rattus norvegicus cytokeratin-18 mRNA, partial cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1507	B,Q	1105	AI229235			ESTs
1510	Q	1646	NM_017224		organic cationic transporter-like 1	organic cationic transporter-like 1
1514	B	1559	NM_012678		Tropomycin 4	Tropomycin 4
1520	H	1659	NM_019165		interleukin 18	interleukin 18
1521	B,Q	1601	NM_013091		Tumor necrosis factor receptor	Tumor necrosis factor receptor
1529	A,G	1599	NM_013082		Ryudocan/syndecan 2	Ryudocan/syndecan 2
1531	A	1655	NM_017300	Bile acid biosynthesis, Taurine and hypotaurine metabolism	bile acid-Coenzyme A dehydrogenase: amino acid n-acyltransferase	bile acid-Coenzyme A dehydrogenase: amino acid n-acyltransferase
1538	E	493	AF039890		Leucine arylaminopeptidase 1	Rat kidney Zn-peptidase aminopeptidase N mRNA, complete cds
1542	G,H	1643	NM_017193		kynurenine aminotransferase II	kynurenine aminotransferase II
1551	K	1633	NM_017084	Glycine, serine and threonine metabolism	Glycine methyltransferase	Glycine methyltransferase
1554	I	625	AI045440		Sialophorin (gpL115, leukosianin, CD43)	Sialophorin (gpL115, leukosianin, CD43)
1561	A,M,O	1621	NM_016995		Complement component 4 binding protein, beta	Complement component 4 binding protein, beta
1562	F,G	267	AA893552			Rattus norvegicus kallistatin mRNA, complete cds
1571	I	1446	U05014			Rattus norvegicus Sprague/Dawley PHAS-I mRNA, complete cds
1572	Q	1046	AI178828			Rattus norvegicus Sprague/Dawley PHAS-I mRNA, complete cds
1579	R	1512	X73411			Rat small nuclear ribonucleoparticle-associated protein (snRNP) mRNA, complete cds, clone Sm51

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1583	A	1448	U07201	Alanine and aspartate metabolism, Nitrogen metabolism	Asparagine synthetase	Asparagine synthetase
1598	C,J	1722	NM_024134		DNA-damage inducible transcript 3	Rattus norvegicus GADD153 mRNA, complete cds
1610	C	1703	NM_022509			Rattus norvegicus survival motor neuron (smn) mRNA, complete cds
1625	I	1588	NM_012924		Cell surface glycoprotein CD44 (hyaluronate binding protein)	Cell surface glycoprotein CD44 (hyaluronate binding protein)
1641	E	1354	E03428		Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1644	G	208	AA891068		Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1653	G	1222	AI233806		Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1661	B,E	1459	U26397	Inositol phosphate metabolism	HHs:inositol polyphosphate-4-phosphatase, type I, 107kD	Rattus norvegicus inositol polyphosphate 4-phosphatase mRNA, complete cds
1690	A,E	46	AA817829			ESTs, Highly similar to MEK binding partner 1 [M.musculus]
1700	P	1486	X03369		tubulin, beta 2	ESTs, Highly similar to TBB1_RAT TUBULIN BETA CHAIN [R.norvegicus],Rat mRNA for beta-tubulin T beta15
1727	C,J	482	AF001417			Rattus norvegicus zinc finger protein mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1728	E,S	1332	D16479	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Phenylalanine metabolism, Valine, leucine and isoleucine degradation	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Rat mRNA for mitochondrial long-chain 3 ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, complete dds
1749	K	1657	NM_017327		GTP-binding protein	GTP-binding protein
1753	A	1462	U39208	Prostaglandin and leukotriene metabolism	HHs:cytochrome P450, subfamily IVF, polypeptide 2	Rattus norvegicus cytochrome P450 4F6 (CYP4F6) mRNA, complete cds
1777	P	1586	NM_012918		Calcium channel alpha 1A	Calcium channel alpha 1A
1795	B,K,Q	1392	L24207		Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
1796	B,K	1392	L24207		Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
1802	H	47	AA817841			ESTs
1805	N	508	AI007824			Rattus rattus guanine nucleotide-releasing protein (mss4) mRNA, complete cds
1809	F	391	AA946503			Rat mRNA for alpha-2u globulin-related protein
1841	C,N	1555	NM_012637		Protein-tyrosine phosphatase	Protein-tyrosine phosphatase
1843	N,Q	1555	NM_012637		Protein-tyrosine phosphatase	Protein-tyrosine phosphatase
1844	A,N	1555	NM_012637		Protein-tyrosine phosphatase	ESTs,Protein-tyrosine phosphatase
1854	M	1382	K02814		K-kininogen, differential splicing leads to HMW Kngk,T-kininogen	K-kininogen, differential splicing leads to HMW Kngk,T-kininogen

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1858	S	1524	Y09333		acyl-CoA thioesterase 1, cytosolic	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase,Rattus norvegicus mRNA for acyl-CoA hydrolase, complete cds
1877	A	1513	X74593	Fructose and mannose metabolism	Sorbitol dehydrogenase	Sorbitol dehydrogenase
1884	L	1340	D50695			Rattus norvegicus mRNA for proteasomal ATPase (Tat-binding protein7), complete cds
1893	P	1495	X51529	Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism	phospholipase A2, group IIA (platelets, synovial fluid)	Rattus norvegicus mRNA for phospholipase A2 precursor, complete cds
1900	A,B,L	48	AA817849			ESTs
1901	L	48	AA817849			ESTs
1903	L	1013	AI177377			ESTs
1919	H	815	AI137856		P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1920	H	1397	M10068		P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1921	H	1351	E01524		P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1929	A	1449	U10357		Hsp:[PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2, MITOCHONDRIAL PRECURSOR	Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) mRNA, complete cds
1930	L	410	AA957202			Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
1957	K	1628	NM_017060		Hras-revertant gene 107	Hras-revertant gene 107
1995	N	492	AF038870	Glycine, serine and threonine metabolism, Methionine metabolism	HMm:betaine-homocysteine methyltransferase	Rattus norvegicus betaine homocysteine methyltransferase (BHMT) mRNA, complete cds
2006	E	1716	NM_022936			R.norvegicus mRNA for cytosolic epoxide hydrolase
2011	P	1610	NM_013173		Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
2012	P	1610	NM_013173		Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
2013	P	1610	NM_013173		Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
2042	Q,R	721	AI101921			ESTs
2043	E,H	1125	AI230171			ESTs
2049	J	417	AA963369			ESTs
2051	S	418	AA963372			ESTs
2065	I	1084	AI227769			ESTs
2101	R	565	AI013667			ESTs
2111	A	750	AI103550			Rattus norvegicus CDK102 mRNA
2113	S	423	AA964275			ESTs, Weakly similar to AF077030_1 hypothetical 43.2 kDa protein [H.sapiens]
2117	R	324	AA925961			Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
2153	E	1475	U75404			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
2154	R	1223	AI233818			ESTs
2164	A	781	AI111413			ESTs
2190	S	420	AA964004			ESTs
2196	A	776	AI105243			ESTs
2216	R	912	AI171745			ESTs
2264	A	821	AI144741			ESTs
2280	H	421	AA964139			EST
2292	E	714	AI101362			ESTs
2310	M	587	AI029969			ESTs
2326	L	432	AA964892			ESTs, Highly similar to CA14_MOUSE COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR [M.musculus]
2335	A	424	AA964302			ESTs
2339	E	1162	AI231798			ESTs
2342	E	425	AA964336			EST
2350	D	426	AA964368			ESTs, Highly similar to TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE [H.sapiens]
2354	L	454	AA997763			ESTs, Highly similar to hypothetical protein [H.sapiens]
2359	N	998	AI177029			ESTs, Highly similar to JU0227 protein-tyrosine kinase [M.musculus]
2368	N	504	AF095741			Rattus norvegicus MG87 mRNA, complete cds
2372	A,L	1130	AI230373			ESTs
2373	O	428	AA964455			ESTs
2383	A,E	429	AA964514			ESTs
2457	S	431	AA964752			EST
2484	A,O	761	AI104675			ESTs

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GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
M_012597	Glycerolipid metabolism	Lipase, hepatic	Lipase, hepatic
009341			ESTs
176590			ESTs
176616			ESTs
M_012967		Intercellular adhesion molecule 1	Intercellular adhesion molecule 1
A965122			ESTs
A891884			ESTs
232103			ESTs
234843			ESTs, Moderately similar to Similarity to Yeast LPG22P protein [C.elegans]
229318			ESTs
M_012603		Avian myelocytomatosis viral (v-myc) oncogene homolog	Avian myelocytomatosis viral (v-myc) oncogene homolog
M_012603		Avian myelocytomatosis viral (v-myc) oncogene homolog	Avian myelocytomatosis viral (v-myc) oncogene homolog
A943886			Rattus norvegicus protein kinase SNK (Snk) mRNA, complete cds
M_012766		Tocopherol transfer protein alpha	Tocopherol transfer protein alpha
A965075			ESTs
M_022515			R.norvegicus (Sprague Dawley) mRNA for ribosomal protein L24
A892918			ESTs
M_012519		Ca++/calmodulin-dependent protein kinase II, delta subunit	Ca++/calmodulin-dependent protein kinase II, delta subunit
37991			ESTs, Highly similar to UGTrel1 [M.musculus]
A997851			ESTs
A944165			ESTs, Highly similar to C10 [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
2763	E	1173	AI232269			ESTs
2781	I	50	AA817925			ESTs
2788	J	939	AI175513			Rattus norvegicus mRNA for phocein protein
2799	A	568	AI013778			ESTs
2801	F	1345	D85435			Rattus norvegicus mRNA for protein kinase C delta-bindig protein, complete cds
2802	F	1345	D85435			Rattus norvegicus mRNA for protein kinase C delta-bindig protein, complete cds
2803	L	437	AA996451			ESTs
2813	S	365	AA945052	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation	HMm:3-hydroxy-3-methylglutaryl-Coenzyme A lyase	R.norvegicus mRNA for 3-hydroxy-3-methylglutaryl CoA lyase
2818	C,D,F	1055	AI179144			ESTs
2838	D	655	AI070511			ESTs, Highly similar to G7A [M.musculus]
2853	I	1579	NM_012838		Cystatin beta	Cystatin beta
2854	I	1579	NM_012838		Cystatin beta	Cystatin beta
2868	E	1171	AI232209			ESTs
2897	C,D	51	AA818039			ESTs
2901	A	603	AI043752			ESTs
2905	A,B	438	AA996727			ESTs
2911	A	597	AI030835			ESTs
2915	R	439	AA996782			ESTs
2932	R	1204	AI233288			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
2933	E	1665	NM_019204			ESTs, Highly similar to beta-site APP cleaving enzyme [R.norvegicus]
2938	C	440	AA996883			ESTs
2993	A	971	AI176492			ESTs, Highly similar to AF188297_1 TGF-beta receptor binding protein [M.musculus]
3023	G	885	AI170795			ESTs
3062	D	468	AA998857			EST, Weakly similar to CBPB_RAT CARBOXYPEPTIDASE B PRECURSOR [R.norvegicus]
3073	A,E,O	1213	AI233494			ESTs
3074	A,E,O	1213	AI233494			ESTs
3075	A,O	1213	AI233494			ESTs
3080	H	242	AA892553		HHs:signal transducer and activator of transcription 1, 91kD	Rattus norvegicus signal transducer and activator of transcription 1 (Stat1) mRNA, complete cds
3091	E	1260	AI236027			ESTs
3099	S	1113	AI229680	Oxidative phosphorylation, Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NADH:ubiquinone oxidoreductase NDUFS3 subunit [H.sapiens]
3121	A,B,E	510	AI008160			ESTs, Moderately similar to AF151841_1 CGI-83 protein [H.sapiens]
3131	A	256	AA893032			ESTs
3138	I	1047	AI178850			ESTs
3139	J	540	AI010618			ESTs
3143	E,H	1180	AI232408			ESTs
3145	A	444	AA997237			EST
3175	S	447	AA997414			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3189	A	448	AA997438			ESTs, Moderately similar to LDL receptor member LR3 [M.musculus]
3203	C	1624	NM_017039		Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
3207	A	449	AA997466			ESTs
3219	E	767	AI105065			ESTs, Highly similar to PNAD_MOUSE PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE [M.musculus]
3233	L	53	AA818105			ESTs, Moderately similar to Unknown gene product [H.sapiens]
3250	M	455	AA997765			Rattus norvegicus fibrillin-1 mRNA, complete cds
3253	F	1652	NM_017282		proteasome (prosome, macropain) subunit, alpha type 5	proteasome (prosome, macropain) subunit, alpha type 5
3260	S	571	AI013875			ESTs
3266	L	915	AI171948			ESTs
3279	S	747	AI103224			ESTs, Weakly similar to putative short-chain dehydrogenase/reductase [R.norvegicus]
3280	C	1083	AI227699			ESTs
3292	M,N	1325	D00753			Rat mRNA for contrapsin-like protease inhibitor related protein (CPi-26)
3365	A,B	518	AI008919			ESTs
3381	K	254	AA892993			ESTs
3418	A,C,D	936	AI175475			ESTs, Highly similar to NHPX_RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus]
3430	J	1441	S85184		Cathepsin L	Cathepsin L

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3439	S	255	AA893000			ESTs, Highly similar to KIAA0564 protein [H.sapiens]
3452	M,N	452	AA997721			Rattus norvegicus orphan chemokine receptor mRNA, complete cds
3486	H	869	AI170313			ESTs
3504	A,B	760	AI104659			Rattus norvegicus mRNA for R-RCD1, complete cds
3510	K	963	AI176423			ESTs, Highly similar to ZO1_MOUSE TIGHT JUNCTION PROTEIN ZO-1 [M.musculus]
3513	S	1639	NM_017177	Glycerolipid metabolism	choline/ethanolamine kinase	choline/ethanolamine kinase
3549	H,I	1385	L11319			Rat signal peptidase mRNA, complete cds
3558	S	463	AA998461			EST
3570	O	464	AA998510			ESTs, Weakly similar to RET1_RAT RETINOL-BINDING PROTEIN I, CELLULAR [R.norvegicus]
3587	J	1078	AI180253			ESTs
3617	N	1259	AI236021			Rattus norvegicus gene for hepatocarcinogenesis-related transcription factor (HTF), complete cds
3626	P	950	AI176031			ESTs, Weakly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]
3631	S	302	AA924460			ESTs, Highly similar to Opa-interacting protein OIP2 [H.sapiens]
3660	B	467	AA998833			ESTs
3708	M	469	AA999060			EST

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3710	B,Q	470	AA999064			ESTs
3713	A,N	791	AI112571			ESTs
3720	S	471	AA999138			ESTs
3722	N	457	AA997979			ESTs
3730	N	460	AA998234			EST
3743	S	1335	D30666			Rat mRNA for brain acyl-CoA synthetase II, complete cds
3749	P	461	AA998276			EST
3776	Q	1679	NM_019354		Uncoupling protein 2, mitochondrial	Uncoupling protein 2, mitochondrial
3803	L,R	884	AI170773			Rattus norvegicus 250 kDa estrous-specific protein mRNA, partial cds
3816	J	1219	AI233729			ESTs, Highly similar to PSD5_HUMAN 26S PROTEASOME SUBUNIT S5B [H.sapiens]
3822	A	288	AA900863			ESTs, Weakly similar to nuclear RNA helicase [R.norvegicus]
3823	A	1196	AI233147			ESTs, Weakly similar to nuclear RNA helicase [R.norvegicus]
3831	C,J	1525	Y12635	Oxidative phosphorylation	HMm:ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2	R.norvegicus mRNA for vacuolar adenosine triphosphatase subunit B
3846	O	658	AI070895			ESTs, Weakly similar to similar to acyl-CoA dehydrogenases and epoxide hydrolases [C.elegans]
3849	A	567	AI013745			ESTs, Moderately similar to CGI-147 protein [H.sapiens]
3916	A,F	865	AI169947			ESTs
3917	B	1194	AI232970			ESTs
3929	O	270	AA894233			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3934	A	544	AI011510			ESTs
3959	A	292	AA901338			ESTs, Highly similar to IF2B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT [H.sapiens]
3969	A	1001	AI177055			ESTs
3972	Q	300	AA924307			ESTs
3976	E	61	AA818264			ESTs, Weakly similar to similar to GTPase-activating proteins [H.sapiens]
3981	A	554	AI012235			ESTs
3995	A	545	AI011678			ESTs
4017	A	63	AA818287			ESTs
4026	B,Q	1225	AI233835			ESTs
4048	I	139	AA851814			Rattus norvegicus osteoactivin mRNA, complete cds
4049	I	784	AI112012			Rattus norvegicus osteoactivin mRNA, complete cds
4082	O	624	AI045256			ESTs
4084	A	512	AI008504			ESTs
4092	L	1095	AI228723	Glycolysis/ Gluconeogenesis	HHs:phosphoglycerate mutase 1 (brain)	R.norvegicus phosphoglycerate mutase B isozyme (PGAM) mRNA, complete cds
4097	I	1037	AI178635			ESTs
4119	J	720	AI101901			ESTs
4127	H	1057	AI179206			ESTs
4143	A	786	AI112107			ESTs
4157	E	525	AI009481			ESTs, Weakly similar to putative [C.elegans]
4168	E	527	AI009654			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4178	I	170	AA859536			ESTs
4179	A,C,E,R	1132	AI230431			ESTs
4193	A,C,D,E,F,I	923	AI172274			ESTs, Weakly similar to I37195 AU-specific RNA-binding protein / enoyl-CoA hydratase [H.sapiens]
4199	G	1425	M83143		Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase)	Rat beta-galactoside-alpha 2,6-sialyltransferase mRNA
4207	F	371	AA945591			ESTs, Weakly similar to JC5105 stromal cell-derived factor 2 - mouse [M.musculus]
4224	G	1415	M31322			Rat sperm membrane protein (YWK-II) mRNA, 3' end
4231	R	1159	AI231763			Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds
4234	H	1685	NM_021577			Rattus norvegicus mRNA for AIF-C1, complete cds
4250	B	76	AA818700			ESTs
4271	S	321	AA925603			ESTs, Moderately similar to AF153605_1 androgen induced protein [H.sapiens]
4272	S	1152	AI231309			ESTs, Moderately similar to AF153605_1 androgen induced protein [H.sapiens]
4281	A,G	1663	NM_019192		selenoprotein P, plasma, 1	selenoprotein P, plasma, 1
4290	S	1323	AJ224120			Rattus norvegicus peroxisomal membrane protein Pmp26p (Peroxin-11)
4291	A,H	79	AA818741			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4312	K	480	AB010635			Rattus norvegicus mRNA for carboxylesterase precursor, complete cds
4314	G,M	483	AF010597			Rattus norvegicus bile salt export pump (spgp) mRNA, complete cds
4318	F	474	AB005900			Rattus norvegicus mRNA for endothelial receptor for oxidized low-density lipoprotein, complete cds
4327	I	498	AF063447			Rattus norvegicus nuclear RNA helicase mRNA, complete cds
4330	A,C,D,E	80	AA818747			Rattus norvegicus stromal cell-derived factor-1 gamma mRNA, complete cds
4348	E	874	AI170447			Rattus norvegicus mRNA for norepinephrine transporter b (rNETb), complete cds
4360	A	1358	H31813			ESTs
4371	E	295	AA924196			ESTs
4426	I	3	AA685974			ESTs
4438	S	2	AA684919			ESTs
4440	A,O	1189	AI232643			ESTs
4473	A	229	AA891965			ESTs
4504	Q	1725	NM_024159			Rattus norvegicus DOC-2 p59 isoform mRNA, complete cds
4520	O	751	AI103694	Oxidative phosphorylation, Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	ESTs, Moderately similar to NADH-ubiquinone oxidoreductase subunit CI-B8 [H.sapiens]
4553	A,C	999	AI177038			ESTs
4576	K	1049	AI178872			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4588	K	477	AB009636			Rattus norvegicus mRNA for phosphoinositide 3-kinase, complete cds
4592	C,D	1680	NM_019356		eukaryotic translation initiation factor 2, subunit 1 (alpha)	eukaryotic translation initiation factor 2, subunit 1 (alpha)
4610	E	1075	AI179991			ESTs
4650	G	718	AI101582			ESTs
4670	A,N	1217	AI233714			ESTs
4674	O	279	AA899847			EST
4679	L	585	AI029847			ESTs, Highly similar to IRF3_MOUSE INTERFERON REGULATORY FACTOR 3 [M.musculus]
4719	A	1087	AI228265			ESTs
4725	L	282	AA900290			ESTs
4759	E	285	AA900553			ESTs
4781	C,D	1228	AI233925			ESTs
4856	I	752	AI103708			ESTs
4868	A	882	AI170763			ESTs
4892	P	611	AI044292			ESTs
4914	A	785	AI112086			ESTs
4929	E	296	AA924236			EST
4931	S	297	AA924261			ESTs, Moderately similar to unknown [H.sapiens]
4933	A,E,P	299	AA924301			EST
4937	A,L	1294	AI237189			ESTs
4940	S	1738	NM_022526			Rattus norvegicus rap7a mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4944	A,F	301	AA924405			ESTs, Moderately similar to NO56_HUMAN NUCLEOLAR PROTEIN NOP56 [H.sapiens]
4951	A	519	AI009026			ESTs
4952	C,J	86	AA818907			ESTs
4969	M	795	AI113008			ESTs, Moderately similar to megakaryocyte stimulating factor [H.sapiens]
5008	A,C	88	AA818921			ESTs
5018	L	306	AA924767			EST
5020	E	307	AA924768			ESTs, Weakly similar to MRJ [M.musculus]
5027	A	308	AA924793			ESTs
5038	E	846	AI169239			ESTs
5046	A,L	1303	AI237855			ESTs
5052	R	1270	AI236302			ESTs, Weakly similar to TTHY_RAT TRANSTHYRETIN PRECURSOR [R.norvegicus]
5059	Q	1288	AI236947			ESTs
5091	E	699	AI073092			ESTs
5110	E,M	317	AA925274			ESTs
5111	E	397	AA955729			EST,ESTs
5175	A	90	AA818951	Glycolysis/ Gluconeogenesis, Purine metabolism, Pyruvate metabolism	Pyruvate kinase, muscle	Pyruvate kinase, muscle
5219	A	322	AA925807			ESTs
5235	F	829	AI145569			ESTs, Moderately similar to BcDNA.GH02974 [D.melanogaster]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
5291	M	1190	AI232700			ESTs
5331	I	91	AA818996	Aminoacyl-tRNA biosynthesis, Glutamate metabolism	HHs:glutaminyl-tRNA synthetase	ESTs, Moderately similar to SYQ_HUMAN GLUTAMINYL-TRNA SYNTHETASE [H.sapiens]
5339	E,M	911	AI171727	Nicotinate and nicotinamide metabolism	HMm:nicotinamide N-methyltransferase	ESTs, Weakly similar to PNMT [R.norvegicus]
5381	R	1038	AI178734			ESTs
5384	A,B,F	207	AA891041			ESTs
5434	E	1380	K01878		Proopoimelanocortin, beta (endorphin, beta)	Rat proopiomelanocortin (POMC) gene
5437	F	407	AA956910			ESTs
5461	A	613	AI044338			EST
5464	B,O	614	AI044345			ESTs, Highly similar to AF172275_1 FUS2 [M.musculus]
5489	C,J	914	AI171795			ESTs
5492	G	1336	D38061	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs,UDP-glucuronosyltransferase 1 family, member 1
5493	G,O	1433	S56936	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs,UDP-glucuronosyltransferase 1 family, member 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
5504	D	1165	AI231805			ESTs, Weakly similar to NUML_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT [M.musculus]
5518	S	617	AI044550			EST
5565	S	377	AA945879			ESTs
5602	S	1187	AI232611			ESTs, Weakly similar to mitochondrial very-long-chain acyl-CoA thioesterase [R.norvegicus]
5608	R	93	AA819041			ESTs
5616	M,S	1731	NM_019143		Fibronectin 1	Fibronectin 1
5622	A	1731	NM_019143		Fibronectin 1	Fibronectin 1
5687	P	705	AI101006			ESTs
5696	L	621	AI045116			ESTs
5733	C	1424	M81855		P-glycoprotein 2/ multidrug resistance 1b,P-glycoprotein/multidrug resistance 1	P-glycoprotein/multidrug resistance 1
5740	L	680	AI072092			ESTs, Moderately similar to DYNC_HUMAN DYNACTIN, 50 KD ISOFORM [H.sapiens]
5748	A	1650	NM_017279		proteasome (prosome, macropain) subunit, alpha type 2	proteasome (prosome, macropain) subunit, alpha type 2
5749	A,H	1650	NM_017279		proteasome (prosome, macropain) subunit, alpha type 2	proteasome (prosome, macropain) subunit, alpha type 2
5754	L,R	133	AA850738			ESTs
5780	C,D	1019	AI177869			ESTs, Weakly similar to DRAL [R.norvegicus]
5794	C	1212	AI233480			ESTs
5795	E	626	AI045441			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
5813	A	1026	AI178231			ESTs
5820	J	1285	AI236771			ESTs
5824	K	627	AI045555			EST
5863	A	95	AA819111			ESTs
5867	A,C,D	158	AA858953	Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis	HHs:asparaginyl-tRNA synthetase	ESTs, Highly similar to SYN_HUMAN ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]
5885	I	1322	AJ223184			Rattus norvegicus mRNA for DORA protein
5887	S	1053	AI179099		vanin 1	ESTs, Moderately similar to Vanin-1 [M.musculus]
5899	A,D,F	867	AI170038			ESTs
5920	G	843	AI169163			ESTs
5923	A	65	AA818355			ESTs
5926	C	1017	AI177638			ESTs, Moderately similar to M phase phosphoprotein 10 [H.sapiens]
5930	E	42	AA817688			ESTs
5932	J	756	AI104254			ESTs
5934	A,F	43	AA817695			ESTs, Highly similar to 2008147C protein RAKd [R.norvegicus]
5937	J	908	AI171684			ESTs
5943	A	1005	AI177105			ESTs
5953	H	893	AI171231			Rattus norvegicus amino acid transporter system A (ATA2) mRNA, complete cds
5966	H	89	AA818947			ESTs
5993	R	820	AI144612			ESTs
5998	G	1317	AI639501			ESTs
6003	E	54	AA818107			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6007	A	55	AA818123			ESTs
6012	D	56	AA818139			ESTs
6013	N	1634	NM_017096		C-reactive protein	C-reactive protein
6015	A,O	57	AA818158			ESTs
6016	A,C,D	58	AA818163			EST
6017	A	1676	NM_019292	Nitrogen metabolism	carbonic anhydrase 3	carbonic anhydrase 3
6018	E,N	96	AA819140	Nitrogen metabolism	carbonic anhydrase 3	carbonic anhydrase 3
6026	E	59	AA818211			EST
6032	E	60	AA818258			ESTs
6033	A	1195	AI233081			ESTs
6037	A	64	AA818288			ESTs
6039	D	330	AA942716			ESTs, Highly similar to HN1 [M.musculus]
6060	A,O	77	AA818702			ESTs
6066	E	83	AA818781			ESTs
6072	A,B,E,F	1093	AI228630			ESTs, Weakly similar to Similarity to litosperm LEC14B protein [C.elegans]
6085	C	916	AI171990			ESTs, Moderately similar to axonemal dynein heavy chain [H.sapiens]
6101	R	881	AI170752			ESTs
6132	A,C,D	94	AA819055			EST
6143	A,C	771	AI105167			ESTs, Moderately similar to selenium-binding protein [H.sapiens]
6151	G	98	AA819199			EST
6153	G	203	AA875531			Rattus norvegicus pro-alpha-2(I) collagen (col1a2) mRNA, complete cds
6155	G	715	AI101443			Rattus norvegicus pro-alpha-2(I) collagen (col1a2) mRNA, complete cds
6188	E	82	AA818774			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6189	B,E,G	1023	AI178027			ESTs, Weakly similar to GTP_RAT GLUTATHIONE S-TRANSFERASE P [R.norvegicus]
6190	A	107	AA819812			ESTs
6193	I	1161	AI231797			ESTs
6198	M	109	AA819840			ESTs
6200	P	110	AA819853		HHs:lymphotoxin beta (TNF superfamily, member 3)	ESTs, Highly similar to TNFC_MOUSE LYMPHOTOXIN-BETA [M.musculus]
6213	N	726	AI102190			ESTs
6222	N	68	AA818474			ESTs
6226	A	70	AA818521			ESTs
6236	B,E,P	75	AA818627			EST, Moderately similar to ISI1_RAT INSULIN-INDUCED PROTEIN 1 [R.norvegicus]
6272	L	875	AI170617			ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]
6291	H	822	AI144797			ESTs
6292	S	422	AA964181			ESTs
6295	N	103	AA819672			EST
6321	A,J	712	AI101256			ESTs, Weakly similar to AIF-C1 [R.norvegicus]
6322	A	85	AA818801			EST
6330	H	873	AI170426			ESTs
6366	A,E,H	152	AA858716			Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds
6380	A,C,D	153	AA858758			ESTs, Weakly similar to dJ413H6.1.1 [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6409	E	156	AA858910			ESTs
6410	A	157	AA858926			ESTs
6431	K,P	159	AA859085			EST
6439	S	636	AI058436			ESTs
6440	R	160	AA859130			ESTs
6443	A	161	AA859150			ESTs
6473	A	1002	AI177091			ESTs
6477	N	1371	J00735		Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
6479	K	860	AI169690		Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
6532	B,Q	1232	AI234105			ESTs
6533	E	155	AA858852			ESTs, Moderately similar to hypothetical protein [H.sapiens]
6541	O	740	AI102905			ESTs
6549	O	949	AI176002	Folate biosynthesis	Folylpolyglutamate synthase	ESTs, Highly similar to S65755 tetrahydrofolylpolyglutamate synthase [M.musculus]
6553	S	594	AI030271			ESTs
6554	A	505	AF097723			Rattus norvegicus liver annexin-like protein (LAL) mRNA, complete cds
6582	L	910	AI171726			ESTs, Weakly similar to ESR1_RAT ESTROGEN RECEPTOR [R.norvegicus]
6585	F	1695	NM_022266			Rattus norvegicus mRNA for connective tissue growth factor, complete cds
6604	A,O	1104	AI229192			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6613	A,F	117	AA848758	Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Tryptophan metabolism, Valine, leucine and isoleucine degradation	HMm:hydroxylacyl-Coenzyme A dehydrogenase	Rattus norvegicus L-3-hydroxyacyl-CoA dehydrogenase precursor (HAD) mRNA, complete cds; nuclear gene for mitochondrial product
6615	A	335	AA942889			ESTs, Weakly similar to putative type III alcohol dehydrogenase [D.melanogaster]
6632	A	1246	AI235277			ESTs
6633	A,N	1098	AI228931			ESTs
6640	A	716	AI101500			ESTs
6667	K	905	AI171646			ESTs
6673	E	612	AI044325			Rattus norvegicus mRNA for N-cadherin, complete cds
6676	L	143	AA851967			ESTs
6677	S	542	AI011471			ESTs
6682	A	1168	AI232065			ESTs
6686	R	952	AI176130			ESTs
6761	A	513	AI008699			ESTs, Highly similar to methyl-CpG binding domain-containing protein MBD3 [M.musculus]
6789	O,R	459	AA998207			ESTs
6796	C	735	AI102753			ESTs
6798	E	857	AI169619			ESTs
6801	A,E,K	536	AI010316			ESTs
6804	E	509	AI007877			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6814	E	717	AI101534			EST,Rattus norvegicus Mdk mRNA for midkine, complete cds
6820	A,D	1133	AI230439			ESTs
6821	E,L	990	AI176841			ESTs
6824	A,C,D,F,I	104	AA819709			ESTs
6825	A,B,Q,S	631	AI045972			ESTs
6855	A,L	899	AI171370			ESTs
6861	H,R	995	AI176970			ESTs
6879	I	907	AI171674			ESTs
6892	J	33	AA800551			Rattus norvegicus DnaJ-like protein (RDJ1) mRNA, complete cds
6911	D	1343	D85035	Pantothenate and CoA biosynthesis,Pyrimidine metabolism,beta-Alanine metabolism	HHs:dihydropyrimidine dehydrogenase	Rattus norvegicus mRNA for dihydropyrimidine dehydrogenase, complete cds
6919	N	537	AI010461			ESTs
6975	O	953	AI176229			ESTs
7003	A,L	593	AI030259			ESTs, Weakly similar to Dreg-2 protein [D.melanogaster]
7036	C,J	1164	AI231801			ESTs, Weakly similar to TERA_RAT TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE [R.norvegicus]
7056	B,M	543	AI011503			ESTs
7062	A	1533	NM_012495	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis,Pentose phosphate cycle	Aldolase A, fructose-bisphosphate	Aldolase A, fructose-bisphosphate

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
7063	A,C,D	1533	NM_012495	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis,Pentose phosphate cycle	Aldolase A, fructose-bisphosphate	Aldolase A, fructose-bisphosphate
7064	A,C	1533	NM_012495	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis,Pentose phosphate cycle	Aldolase A, fructose-bisphosphate	Aldolase A, fructose-bisphosphate
7111	R	108	AA819816			ESTs
7113	A	868	AI170260			ESTs
7122	Q	809	AI137468			ESTs
7161	C	1209	AI233407			ESTs
7176	Q	1306	AI639029			ESTs
7196	P	1585	NM_012904		Annexin 1 (p35) (Lipocortin 1)	Annexin 1 (p35) (Lipocortin 1)
7199	C,D	562	AI013044			ESTs
7225	M	564	AI013657			ESTs
7243	A,C	1218	AI233717			ESTs
7262	D,L	946	AI175833			ESTs
7271	C	1115	AI229739			ESTs
7295	S	572	AI013876			ESTs
7299	A	573	AI013911			ESTs, Weakly similar to CIRP [R.norvegicus]
7301	J	111	AA819854			ESTs
7352	A	577	AI028973			ESTs, Weakly similar to AF165892_1 RNA-binding protein SiahBP [R.norvegicus]
7362	L	578	AI029026			ESTs
7403	C,D	579	AI029212			EST

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
7414	C,D	813	AI137586			ESTs, Highly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens]
7420	S	580	AI029291			ESTs, Highly similar to ClpX-like protein [H.sapiens]
7451	E,N	581	AI029450			ESTs, Moderately similar to SYEP_HUMAN MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [H.sapiens]
7497	O	849	AI169302	Sphingophospholipid biosynthesis	HMm:sphingomyelin phosphodiesterase 1, acid lysosomal	ESTs, Moderately similar to sphingomyelin phosphodiesterase 1, acid lysosomal [H.sapiens]
7517	S	582	AI029709			ESTs
7528	H	749	AI103548			ESTs, Highly similar to AF115778_1 short coiled coil protein SCOCO [M.musculus]
7531	A	1298	AI237614			ESTs
7537	E	584	AI029829			ESTs
7552	E,G,I	629	AI045802			EST
7582	A	588	AI029996			ESTs
7584	O	601	AI043724			ESTs
7586	L	589	AI030024			ESTs
7602	I	1320	AJ001929			Rattus norvegicus mRNA for of CBP-50 protein
7617	A	591	AI030170			ESTs
7665	F	596	AI030668			ESTs
7681	A	595	AI030449			ESTs, Moderately similar to methyltransferase related protein [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
7684	O	592	AI030242			ESTs
7690	I	1700	NM_022284			Rattus norvegicus uroguanylin mRNA, complete cds
7697	A,M	992	AI176942			ESTs
7743	P	651	AI070233			ESTs
7784	A	1570	NM_012789		Dipeptidyl peptidase 4	Dipeptidyl peptidase 4
7785	A,C	1570	NM_012789		Dipeptidyl peptidase 4	Dipeptidyl peptidase 4
7806	J	67	AA818421			ESTs
7858	M,P	599	AI043654			EST
7868	A	711	AI101229			ESTs
7887	C,D	823	AI144832	Aminoacyl-tRNA biosynthesis,Arginine and proline metabolism	HHs:arginyl-tRNA synthetase	ESTs, Moderately similar to SYR_HUMAN ARGINYL-TRNA SYNTHETASE [H.sapiens]
7888	A,C,D	1215	AI233583	Aminoacyl-tRNA biosynthesis,Arginine and proline metabolism	HHs:arginyl-tRNA synthetase	ESTs, Moderately similar to SYR_HUMAN ARGINYL-TRNA SYNTHETASE [H.sapiens]
7892	F	1102	AI229172			ESTs, Weakly similar to FIBA_RAT FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR [R.norvegicus]
7893	A	604	AI043761			EST
7903	A,E,F	605	AI043805			ESTs
7916	E	606	AI043855	Sterol biosynthesis	HMm:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	ESTs, Highly similar to sterol-C5-desaturase [M.musculus]
7918	A	1069	AI179750			ESTs
7927	A,H,O	831	AI145931	Aminosugars metabolism	HHs:UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	R.norvegicus mRNA for UDP-N-acetyl-D glucosamine-2-epimerase

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
7935	C	607	AI043945	Porphyrin and chlorophyll metabolism	HMm:ferrochelatase	ESTs
7936	A	202	AA875495			ESTs
7967	L	1124	AI230134	Purine metabolism	HHs:adenylate cyclase 9	ESTs
8017	P	633	AI058341			EST, Weakly similar to putative integral membrane transport protein [R.norvegicus]
8053	K	932	AI175033			ESTs
8054	R	1099	AI228959			ESTs
8079	B,M,Q	637	AI058581			ESTs
8107	G	1318	AI639534			ESTs, Moderately similar to PROP_MOUSE PROPERDIN [M.musculus]
8124	E	742	AI103071		Protein tyrosine phosphatase, gamma (provisional HGM11 symbol)	ESTs
8152	I	1478	U77038		HMm:hemopoietic cell phosphatase	Rattus norvegicus protein-tyrosine phosphatase (SHP-1) mRNA, complete cds
8173	E	450	AA997699			ESTs
8177	S	638	AI058603			ESTs
8215	L	909	AI171692			Rat ferritin light chain subunit, mRNA,Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds
8273	P	765	AI104908			ESTs
8274	B	641	AI059270			EST, Weakly similar to hypothetical protein [H.sapiens]
8310	P	1048	AI178868			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
8314	J	642	AI059386			ESTs
8315	S	643	AI059389	Alanine and aspartate metabolism,Purine metabolism	HMm:adenylosuccinate synthetase 1, muscle	ESTs, Highly similar to PUA1_MOUSE ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME [M.musculus]
8317	A,E	234	AA892234	Glutathione metabolism	HHs:microsomal glutathione S-transferase 3	ESTs, Moderately similar to microsomal glutathione S-transferase 3 [H.sapiens]
8356	G	645	AI059543			EST
8387	A	962	AI176365			ESTs
8477	A	1056	AI179167			ESTs
8515	N	127	AA849917			ESTs
8522	M,P	647	AI060071			ESTs
8549	A,F,H	1216	AI233639			ESTs
8592	G	1364	H33491			Rattus norvegicus sterol delta 8-isomerase (RSI) mRNA, complete cds
8597	B,H	72	AA818593			Rattus norvegicus phosphatidate phosphohydrolase type 2 mRNA, complete cds
8600	A	640	AI058956			ESTs
8630	A	529	AI009677			ESTs
8661	J	73	AA818604		Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8662	J	115	AA848563		Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8663	J	1527	Z27118		Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
8664	J	1530	Z75029		Heat shock protein 70-1	ESTs,Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8665	J	675	AI071965		Heat shock protein 70-1	ESTs,Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8692	A	610	AI044247			ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]
8700	E,M	634	AI058388			ESTs
8709	R	1185	AI232534			ESTs, Weakly similar to DnaJ homolog 2 [R.norvegicus]
8715	N	648	AI069920			ESTs
8728	R	74	AA818615			ESTs
8730	H	1028	AI178483			ESTs
8735	H	697	AI073047			Rattus norvegicus clone Pr2 unknown mRNA
8766	A	549	AI012085			ESTs, Weakly similar to thyroid hormone responsive protein [R.norvegicus]
8820	S	650	AI070152			ESTs
8829	A	1567	NM_012749		Nucleolin	Nucleolin
8864	P	652	AI070319			ESTs
8872	G,K	134	AA851050			ESTs
8880	A	824	AI144936			ESTs
8886	D	1221	AI233766			ESTs, Highly similar to Ki antigen [M.musculus]
8905	K	790	AI112511			ESTs
8928	I	212	AA891221			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
8946	A	656	AI070611			ESTs
8984	J	1735	NM_022539		Hsp:METHIONINE AMINOPEPTIDASE 2	Rattus norvegicus initiation factor 2 associated 67 kDa protein (p67) mRNA, complete cds
8993	R	948	AI175997			ESTs
9012	A	657	AI070879			EST
9015	K	1239	AI234810			ESTs
9016	A,B,C,D,E	659	AI070903			EST
9053	A	249	AA892861			ESTs
9063	A	1197	AI233162			ESTs
9072	G	942	AI175635			ESTs
9079	P	667	AI071251			ESTs
9128	L	903	AI171611			ESTs
9148	B	516	AI008813			ESTs
9164	H	1565	NM_012726		Spinocerebellar ataxia type 1	ESTs
9166	E	807	AI137406			ESTs
9170	E	993	AI176947			ESTs
9181	C,D	1071	AI179870			ESTs
9190	H	702	AI100835			ESTs
9191	A	681	AI072107			EST, Weakly similar to PE2R_RAT 20-ALPHA-HYDROXYSTEROID DEHYDROGENASE [R.norvegicus]
9192	E	805	AI137345			ESTs
9223	Q	1417	M36151			Rat MHC class II RT1.B beta gene, encoding cell surface glycoprotein beta chain,Rat mRNA for MHC class II antigen RT1.B-1 beta-chain,Rattus norvegicus MHC class II antigen RT1.B beta chain mRNA, partial cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
9245	A	684	AI072278			ESTs
9267	Q	685	AI072384			ESTs, Moderately similar to human formiminotransferase cyclodeaminase [H.sapiens]
9326	A	799	AI136514			ESTs, Moderately similar to SPIN [H.sapiens]
9331	A,C,D	689	AI072633			ESTs
9336	A	691	AI072643			ESTs
9372	S	692	AI072712			ESTs
9373	S	802	AI136714			ESTs
9374	R	854	AI169557			ESTs, Highly similar to CDN6_MOUSE CYCLIN-DEPENDENT KINASE 6 INHIBITOR [M.musculus]
9399	A	693	AI072812			ESTs
9402	O,R	101	AA819383			ESTs
9423	S	1556	NM_012649		Ryudocan/syndecan 4	Ryudocan/syndecan 4
9424	N	1556	NM_012649		Ryudocan/syndecan 4	Ryudocan/syndecan 4
9425	A	27	AA800059		Ryudocan/syndecan 4	Ryudocan/syndecan 4
9432	E	695	AI072914			EST
9475	A,O	698	AI073059			ESTs
9486	L	69	AA818490			ESTs
9541	A	1704	NM_022542			Rat rhoB gene mRNA, complete cds
9572	R	660	AI071162			ESTs
9583	A	664	AI071185			ESTs
9595	B,E,Q	800	AI136630			ESTs
9598	E	1365	H33832			ESTs
9603	E	666	AI071227			ESTs
9621	O	937	AI175486		ribosomal protein S7	Rat PRRHIS8 mRNA for ribosomal protein S8

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
9627	A	840	AI169041			ESTs
9635	N	676	AI071967			ESTs, Weakly similar to Y281_HUMAN HYPOTHETICAL PROTEIN KIAA0281 [H.sapiens]
9668	K	669	AI071538			ESTs
9674	L	1044	AI178784			ESTs
9697	K	671	AI071642			EST
9712	B,E	988	AI176836			ESTs, Weakly similar to F25H5.6 [C.elegans]
9754	A	788	AI112194			ESTs
9766	R	672	AI071858			ESTs
9775	L	124	AA849767			Rattus norvegicus brain-enriched SH3-domain protein mRNA, complete cds
9784	C	710	AI101226			ESTs
9796	C	677	AI071990			Rattus norvegicus pEachy mRNA, complete cds
9800	R	678	AI072014			ESTs, Weakly similar to AF165892_1 RNA-binding protein SiahBP [R.norvegicus]
9826	A,M	228	AA891950			ESTs
9889	A	618	AI044621			EST
9905	A,G	221	AA891774			ESTs
9925	S	620	AI044925			ESTs
9969	K	622	AI045195			EST
9977	M	623	AI045253			EST
10002	K	816	AI137988			ESTs, Highly similar to myosin X [M.musculus]
10016	F,I	1673	NM_019289		Actin-related protein complex 1b	Actin-related protein complex 1b
10019	J	1043	AI178756			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
10093	G	639	AI058746			EST
10109	A	1502	X58465		Ribosomal protein S5	Ribosomal protein S5
10176	A	102	AA819530			Rattus norvegicus E-septin long form mRNA, complete cds
10184	E	1363	H33426			ESTs
10187	E	985	AI176781			ESTs
10200	L	644	AI059444			ESTs
10248	A	1574	NM_012797		Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)
10306	I	506	AF100470			Rattus norvegicus SERP1 mRNA, complete cds
10378	F	1205	AI233300		Complement component 5	ESTs, Moderately similar to CO5_HUMAN COMPLEMENT C5 PRECURSOR [H.sapiens]
10394	R	337	AA943564			ESTs
10509	A	1696	NM_022268	Starch and sucrose metabolism	HHs:phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	R.norvegicus gene for glycogen phosphorylase (liver type)
10533	S	635	AI058430			ESTs, Highly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]
10540	O	269	AA894027			EST
10544	A,B	1341	D63411			Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10545	A	1455	U21871			Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10549	C,D,E	39	AA801255			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
10593	R	876	AI170673			ESTs
10594	E	704	AI100878			ESTs, Highly similar to EST00098 protein [H.sapiens]
10611	O	1018	AI177790			ESTs
10667	N	1273	AI236366			Rattus norvegicus RNA-binding protein SiahBP mRNA, partial cds
10790	F,M	602	AI043728			EST
10879	A,N	687	AI072476			ESTs
10984	A,P	842	AI169156			ESTs, Weakly similar to HP33 [R.norvegicus]
11021	A,N	106	AA819767			ESTs
11039	G	1705	NM_022543			Rattus norvegicus steroid sensitive gene 1 protein (SSG-1) mRNA, complete cds
11048	E	668	AI071456			EST, Moderately similar to AF099186_1 EH domain-containing protein EHD1 [M.musculus]
11125	L	673	AI071867			ESTs, Highly similar to phosphatidylserine synthase-2 [M.musculus]
11127	E	674	AI071868			EST
11152	G	1629	NM_017073	Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate-ammonia ligase)	Glutamine synthetase (glutamate-ammonia ligase)

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11153	G	1629	NM_017073	Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate-ammonia ligase)	Glutamine synthetase (glutamate-ammonia ligase)
11157	A,E	1184	AI232494			ESTs
11166	A	40	AA801346			ESTs, Highly similar to KIAA0315 [H.sapiens]
11172	P	338	AA943730			ESTs, Weakly similar to TISB_RAT TIS11B PROTEIN [R.norvegicus]
11174	E	333	AA942745			ESTs
11179	A,H	783	AI111559			ESTs
11205	A,G	919	AI172057			ESTs
11215	E	49	AA817921			ESTs, Moderately similar to weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [C.elegans]
11227	O	541	AI010660			ESTs
11228	A	739	AI102871			ESTs
11235	D	1068	AI179709			ESTs, Weakly similar to similar to C.elegans hypothetical protein CET01H8.1,CEC05C12.3,CEF54D1.5. similar to trp and trp-like proteins [H.sapiens]
11280	R	808	AI137420			ESTs, Moderately similar to hepatoma-derived growth factor [M.musculus]
11315	R	892	AI171229			ESTs, Moderately similar to imogen 44 [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11322	E	526	AI009492			ESTs, Highly similar to Unknown [H.sapiens]
11331	C	828	AI145556			ESTs
11336	R	388	AA946441			ESTs
11354	R	833	AI146215			ESTs
11357	A	835	AI146237			ESTs
11403	A,D,L	889	AI171088	Arginine and proline metabolism,Selenoamino acid metabolism,Urea cycle and metabolism of amino groups,beta-Alanine metabolism	HMm:spermidine synthase	ESTs, Highly similar to SPEE_MOUSE SPERMIDINE SYNTHASE [M.musculus]
11404	A,C,D,L	1291	AI237002	Arginine and proline metabolism,Selenoamino acid metabolism,Urea cycle and metabolism of amino groups,beta-Alanine metabolism	HMm:spermidine synthase	ESTs, Highly similar to SPEE_MOUSE SPERMIDINE SYNTHASE [M.musculus]
11422	Q	26	AA799812			ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]
11423	B,H,Q	26	AA799812			ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11426	H	896	AI171305			ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]
11429	A,G	862	AI169706			ESTs
11438	E	922	AI172189			ESTs
11465	O	1263	AI236084			ESTs, Moderately similar to 41BB_MOUSE 4-1BB LIGAND RECEPTOR PRECURSOR [M.musculus]
11483	J	487	AF020618			ESTs, Moderately similar to progression elevated gene 3 protein [R.norvegicus],Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds
11485	E	1248	AI235348			ESTs, Highly similar to nuclear transcriptional repressor Mph1 [M.musculus]
11492	A	770	AI105145			ESTs
11493	J	1356	H31287			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11494	J	1356	H31287			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11495	J	991	AI176901			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11504	A,B	906	AI171652			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11520	A	443	AA997068			ESTs, Weakly similar to CAG6_RAT CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [R.norvegicus]
11527	A,C,R	1108	AI229307			ESTs
11536	A	984	AI176739			ESTs
11561	C	1200	AI233182			ESTs
11563	A	728	AI102560			ESTs
11576	A	832	AI146177			ESTs
11590	E	78	AA818721			ESTs, Moderately similar to S65785 mel-13a protein - mouse [M.musculus]
11596	M	665	AI071194			ESTs
11608	F	172	AA859633			ESTs
11619	L	701	AI100769			ESTs
11623	E	930	AI172471			ESTs, Highly similar to small EDRK-rich factor 2 [M.musculus]
11625	R	708	AI101167			ESTs, Weakly similar to ARL5_RAT ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5 [R.norvegicus]
11635	A,G	173	AA859645			ESTs
11644	K,O	1247	AI235282			ESTs
11645	F,M	725	AI102093			ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]
11660	C,D	1050	AI178944			ESTs, Highly similar to AF167573_1 protein methyltransferase [M.musculus]
11691	A,E	327	AA926193			Rattus norvegicus mRNA for Sulfotransferase K2

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11693	A,C,D,E,K	836	AI168953			Rattus norvegicus mRNA for Sulfotransferase K2
11700	E	557	AI012574			ESTs
11720	B,O,Q	1174	AI232273			ESTs, Highly similar to RNA cyclase homolog [H.sapiens]
11724	K	736	AI102812			ESTs
11731	P	1544	NM_012561		Follistatin	Follistatin
11742	A,E	713	AI101262			ESTs
11745	A	475	AB006450		translocator of inner mitochondrial membrane 17 kDa, a	translocator of inner mitochondrial membrane 17 kDa, a
11821	O	653	AI070350			ESTs, Weakly similar to DP1_MOUSE POLYPOSIS LOCUS PROTEIN 1 HOMOLOG [M.musculus]
11830	N	1052	AI179093			ESTs
11840	N	1526	Y15068			Rattus norvegicus mRNA for Hsp70/Hsp90 organizing protein
11850	G	1431	R46985			R.norvegicus mRNA for ribosomal protein L10a
11876	L	522	AI009321			ESTs
11893	B	1139	AI230951			ESTs
11904	B,F,M,Q	1344	D85183		Brain immunoglobulin like protein with tyrosine - based activation motifs,Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)	Brain immunoglobulin like protein with tyrosine - based activation motifs,Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)
11940	F,H	209	AA891108			ESTs
11959	A	217	AA891735			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11960	K	220	AA891740			ESTs, Weakly similar to EPOR_RAT ERYTHROPOIETIN RECEPTOR PRECURSOR [R.norvegicus]
11974	B	363	AA944958			ESTs
12058	R	1393	L25387	Fructose and mannose metabolism,Galactose metabolism,Glycolysis / Gluconeogenesis,Pentose phosphate cycle	Hsp:6-PHOSPHOFRUCTOKINASE, TYPE C	ESTs, Highly similar to K6PP_RAT 6-PHOSPHOFRUCTOKINASE, TYPE C [R.norvegicus]
12064	A	32	AA800429			ESTs
12087	A	1683	NM_020082		ribonuclease 4	ribonuclease 4
12120	O	121	AA849365			ESTs
12155	K	1370	J00728	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12156	B,G,K	1378	K00996	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12157	K	1379	K01721	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12158	K	1383	L00320	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12160	A,K	66	AA818412	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12185	E	890	AI171094			ESTs, Weakly similar to Cys2/His2 zinc finger protein [R.norvegicus]
12198	R	273	AA899195			Rattus norvegicus replication factor C subunit 2 (RFC2) mRNA, partial cds
12203	L	274	AA899256			ESTs, Weakly similar to translation initiation factor [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
12215	E,S	696	AI072959			ESTs, Moderately similar to monoglyceride lipase [M.musculus]
12216	A	1106	AI229240			ESTs
12277	M,P	342	AA943800			ESTs
12306	A,E,N	360	AA944898			ESTs
12312	A	263	AA893453			ESTs
12314	G	372	AA945596			ESTs, Moderately similar to LECT2 precursor [H.sapiens]
12317	E,R	1237	AI234361			ESTs
12331	A	389	AA946466			ESTs, Weakly similar to cytoplasmic aminopeptidase P [R.norvegicus]
12332	A	389	AA946466			ESTs, Weakly similar to cytoplasmic aminopeptidase P [R.norvegicus]
12361	O	433	AA965031			ESTs
12375	L	798	AI136478			ESTs, Highly similar to p116Rip [M.musculus]
12450	A,P	755	AI103955			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
12463	Q	1191	AI232706			ESTs
12467	S	1193	AI232924			ESTs
12471	A	413	AA957433			ESTs
12551	I	1122	AI230056			ESTs
12577	F,M	779	AI111344			Rattus norvegicus cyclin H mRNA, complete cds
12585	O	380	AA946034			ESTs, Highly similar to AF151803_1 CGI 45 protein [H.sapiens]
12587	A	1120	AI229979			ESTs
12613	I	1357	H31620			ESTs, Highly similar to hypothetical protein [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
12614	C,D,R	933	AI175294			ESTs
12625	R	458	AA998029			ESTs
12655	A,O	1226	AI233836			ESTs
12694	A	416	AA957906			ESTs
12714	P	533	AI010050			ESTs, Weakly similar to LIS1_MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus]
12746	O	548	AI011809			ESTs
12844	N	679	AI072054			ESTs
12848	A,G	251	AA892916			ESTs, Weakly similar to hemomucin [D.melanogaster]
12857	N	694	AI072866			ESTs
12880	E	782	AI111558			ESTs
12928	B,F,R	396	AA955564			ESTs
12946	A,N	1088	AI228291			ESTs
12956	L	1296	AI237580			ESTs
12964	N	1267	AI236227			ESTs
12965	C	792	AI112926			ESTs
12969	J	794	AI112969			ESTs
12999	C	956	AI176276	Aminosugars metabolism	HHs:UDP-N-acteylglucosamine pyrophosphorylase 1	ESTs
13045	M	801	AI136702			ESTs
13055	E	1054	AI179100			ESTs, Highly similar to potential membrane protein C14orf1 [H.sapiens]
13088	A,F,G	266	AA893495			ESTs, Highly similar to CBG_RAT CORTICOSTEROID-BINDING GLOBULIN PRECURSOR [R.norvegicus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13092	O	1158	AI231547		HMm:FK506 binding protein 4 (59 kDa)	ESTs, Weakly similar to PPP5_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13093	B,O	552	AI012177		HMm:FK506 binding protein 4 (59 kDa)	ESTs, Weakly similar to PPP5_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13166	A,R	1039	AI178736			ESTs
13175	E	965	AI176465			ESTs
13203	A,C	1096	AI228728			ESTs
13229	O	154	AA858760			ESTs
13251	C,D,R	1059	AI179264			ESTs, Moderately similar to LZIP-1 and LZIP-2 [M.musculus]
13265	J	719	AI101708			ESTs
13283	A	1598	NM_013078	Arginine and proline metabolism,Urea cycle and metabolism of amino groups	Ornithine carbamoyltransferase	Ornithine carbamoyltransferase
13294	D	1220	AI233731			ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
13332	B,Q	257	AA893080			ESTs
13351	A,H	62	AA818271			ESTs
13353	M,N	938	AI175508			ESTs
13458	C,D,I	934	AI175338			ESTs
13467	C	817	AI138034	Sphingoglycolipid metabolism	HHs:UDP-glucose ceramide glucosyltransferase	Rattus norvegicus UDP-glucose:ceramide glycosyltransferase mRNA, complete cds
13501	R	957	AI176284			ESTs
13534	E	382	AA946187			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13557	B,E,L,N	367	AA945090			ESTs
13568	H	28	AA800169			ESTs
13580	K	1030	AI178507			ESTs
13581	E	1035	AI178602			ESTs
13634	A	1061	AI179381			ESTs, Highly similar to S26812 transcription factor ATF-4 - mouse [M.musculus]
13640	E,H	814	AI137761			ESTs
13646	C,D,E	1509	X62166			ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
13684	A,D,I	81	AA818770			Rattus norvegicus serine protease gene, complete cds
13723	D	1419	M55534		Crystallin, alpha polypeptide 2	ESTs,Rat alpha-crystallin B chain mRNA, complete cds
13749	A	1089	AI228540			ESTs
13757	A	1094	AI228676			ESTs
13762	A,E	1129	AI230326			ESTs
13799	L	947	AI175871			ESTs
13812	R	1101	AI229167			ESTs
13838	R	1111	AI229416			ESTs
13874	C,D	1117	AI229832			ESTs, Weakly similar to KIAA0859 protein [H.sapiens]
13895	M	1127	AI230270			ESTs
13918	E	569	AI013832			ESTs
13926	H	17	AA799601			ESTs
13932	E,H,N	1142	AI230988			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13949	R	1149	AI231193			ESTs, Moderately similar to SEC_HUMAN SEC PROTEIN [H.sapiens]
13963	A,O	1154	AI231388			ESTs
13967	E	1155	AI231439			EST
13992	Q	1281	AI236679			ESTs
14007	A,E	1166	AI231808			ESTs
14016	F	489	AF026505			Rattus norvegicus SH3-containing protein p4015 mRNA, complete cds
14017	F	211	AA891194			Rattus norvegicus SH3-containing protein p4015 mRNA, complete cds
14035	A	1177	AI232328	Tyrosine metabolism	HHs:homogentisate 1,2-dioxygenase (homogentisate oxidase)	ESTs, Highly similar to homogentisate 1,2-dioxygenase [M.musculus]
14051	A,C,D	1183	AI232489			ESTs, Weakly similar to PIR1 [H.sapiens]
14053	E	1243	AI235046			ESTs, Highly similar to DDX6_MOUSE PROBABLE ATP-DEPENDENT RNA HELICASE P54 [M.musculus]
14074	A	1206	AI233323			ESTs
14081	P	1198	AI233164			ESTs
14083	A	1009	AI177181			ESTs
14095	A	1211	AI233468			ESTs
14103	A	1199	AI233172			ESTs, Weakly similar to AF073727_1 EH domain-binding mitotic phosphoprotein [H.sapiens]
14116	S	1207	AI233361			ESTs
14118	A	1208	AI233367			EST

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
14126	E	1062	AI179415		HHs:neurotrophic tyrosine kinase, receptor, type 1	Rattus norvegicus tropomyosin non-muscle isoform NM1 (TPM-gamma) mRNA, complete cds,Rattus norvegicus tropomyosin non-muscle isoform NM3 (TPM-gamma) mRNA, complete cds
14139	H	175	AA859700	Porphyrin and chlorophyll metabolism	HMm:protoporphyrinogen oxidase	EST, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN OXIDASE [M.musculus],EST, Moderately similar to PPOX_HUMAN PROTOPORPHYRINOGEN OXIDASE [H.sapiens]
14171	E	1024	AI178073			ESTs, Weakly similar to cDNA EST yk249b3.5 comes from this gene [C.elegans]
14181	A	1233	AI234107			ESTs
14185	P	177	AA859837	Purine metabolism	HMm:guanine deaminase	Rattus norvegicus guanine aminohydrolase (GAH) mRNA, complete cds
14195	E	775	AI105205			ESTs
14199	K	1234	AI234133			ESTs
14206	A	182	AA859994			ESTs
14208	A,B	723	AI102017			ESTs
14224	C	1140	AI230956			ESTs, Moderately similar to TFG protein [M.musculus]
14242	C,D	1086	AI228197			ESTs
14250	K	21	AA799729	Purine metabolism	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	ESTs,Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
14258	C	1118	AI229902			ESTs
14264	S	1181	AI232409			ESTs, Weakly similar to bK126B4.2 [H.sapiens]
14266	O	1366	H33842			ESTs, Highly similar to phosphoprotein [M.musculus]
14303	L	1148	AI231159			ESTs, Highly similar to KIAA1049 protein [H.sapiens]
14312	A,E	1261	AI236036			ESTs, Moderately similar to UBE-1b [M.musculus]
14330	P	233	AA892146			ESTs
14335	E	1006	AI177115			ESTs
14353	A	171	AA859585			ESTs
14400	F,M	858	AI169620			ESTs
14424	A,J	654	AI070421			ESTs
14449	E	1235	AI234152			ESTs
14458	C,I	826	AI145095			ESTs
14462	C,D	703	AI100871			ESTs
14465	F	253	AA892950			ESTs, Moderately similar to mitochondrial DNA polymerase accessory subunit [M.musculus]
14491	M	535	AI010147			ESTs
14504	M,P	25	AA799804			ESTs
14506	A	1359	H32584			ESTs
14507	S	132	AA850618			ESTs, Highly similar to gp250 precursor [M.musculus]
14512	A,G	793	AI112964			ESTs
14584	A	1250	AI235360			ESTs, Moderately similar to glutathione-S-transferase homolog [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
14595	S	232	AA892128			ESTs
14600	E,R	38	AA801076			ESTs
14619	C,D	1290	AI236989			ESTs
14638	E	803	AI137049			ESTs, Moderately similar to Nibrin [M.musculus]
14693	A,C,D	1240	AI234830			ESTs, Weakly similar to ORF YKR081c [S.cerevisiae]
14738	N,O	997	AI176993			ESTs
14746	A	1252	AI235584			ESTs, Moderately similar to KIAA0922 protein [H.sapiens]
14767	A	1256	AI235895			ESTs
14776	A,E,N	1258	AI235950			ESTs
14840	K	1301	AI237698			ESTs
14869	A	1264	AI236089			ESTs, Weakly similar to /prediction
14882	S	1324	D00362		Esterase 2	Esterase 2
14913	L,R	1274	AI236461			ESTs
14937	A,E	1293	AI237159			ESTs, Highly similar to lipoic acid synthetase [H.sapiens]
14939	C,D	1090	AI228557			ESTs
14958	N	105	AA819744			ESTs
14959	I	1444	U03390			Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds
14960	A,G,O	897	AI171319			ESTs, Highly similar to integrase interactor 1a protein [M.musculus],Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
14962	A,C,D	845	AI169171			ESTs, Highly similar to ENHANCER OF RUDIMENTARY HOMOLOG [M.musculus]
14970	G	218	AA891738	Sulfur metabolism	HHs:sulfite oxidase	Rattus norvegicus sulfite oxidase mRNA, complete cds
14989	O	1012	AI177366		Integrin, beta 1	Integrin, beta 1
14996	A,N	1597	NM_013059	Folate biosynthesis, Glycerolipid metabolism	Tissue-nonspecific ALP alkaline phosphatase	Tissue-nonspecific ALP alkaline phosphatase
14997	A,E,N,O	1597	NM_013059	Folate biosynthesis, Glycerolipid metabolism	Tissue-nonspecific ALP alkaline phosphatase	Tissue-nonspecific ALP alkaline phosphatase
15002	F	851	AI169327			Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
15003	F	851	AI169327			Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
15004	A	1244	AI235224			Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
15015	S	961	AI176363			ESTs
15016	A	925	AI172285			ESTs
15018	E,S	430	AA964688			ESTs
15029	A,C,D,E,P	878	AI170696			ESTs, Weakly similar to development-related protein [R.norvegicus]
15030	L	113	AA848378			ESTs
15032	A,D	1576	NM_012816		Methylacyl-CoA racemase alpha	Methylacyl-CoA racemase alpha
15051	J,R	1271	AI236332	Arginine and proline metabolism	Spermidine / spermine N1-acyltransferase (diamine acetyltransferase)	ESTs, Highly similar to ATDA_MOUSE DIAMINE ACETYLTRANSFERASE [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15055	A	1463	U48220	Fatty acid metabolism, Tryptophan metabolism	HHs:cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing), polypeptide 6	Rattus norvegicus cytochrome P450 2D18 mRNA, complete cds
15057	O	1675	NM_019291	Nitrogen metabolism	carbonic anhydrase 2	carbonic anhydrase 2
15070	H	1081	AI180442	Sterol biosynthesis	HHs:farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	Rat testis-specific farnesyl pyrophosphate synthetase mRNA, complete cds
15080	A	724	AI102045			ESTs, Highly similar to OS-4 protein [H.sapiens]
15089	F	530	AI009752			ESTs
15091	J	1040	AI178740		YY1 transcription factor	ESTs
15097	L,O	1548	NM_012588		Insulin-like growth factor-binding protein (IGF-BP3)	Insulin-like growth factor-binding protein (IGF-BP3)
15113	A,G	941	AI175590			ESTs, Highly similar to dJ1118D24.1c [H.sapiens]
15116	P	190	AA874928			ESTs, Highly similar to sorting nexin 4 [H.sapiens]
15121	E	746	AI103159			Rattus norvegicus interferon-inducible protein 16 mRNA, complete cds
15122	E	1176	AI232303			ESTs, Weakly similar to Sid1669p [M.musculus]
15127	B,K	1434	S56937	Androgen and estrogen metabolism,Pentose and glucuronate interconversions,Porphyrin and chlorophyll metabolism,Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	Rattus norvegicus UDP-glucuronosyltransferase (UGT1.1) gene, complete cds,Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds,UDP-glucuronosyltransferase 1 family, member 1

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15135	A,D	1436	S71021			R.norvegicus mRNA for ribosomal protein L6
15136	A	20	AA799672			R.norvegicus mRNA for ribosomal protein L6
15139	H	818	AI144585			ESTs
15141	E,F	1649	NM_017278		proteasome (prosome, macropain) subunit, alpha type 1	proteasome (prosome, macropain) subunit, alpha type 1
15149	R	164	AA859327			ESTs
15156	A,E	165	AA859341			ESTs, Highly similar to KIAA0418 [H.sapiens]
15162	L	168	AA859350			ESTs
15170	A,H,N	1299	AI237618			ESTs
15171	J	1160	AI231792			ESTs, Moderately similar to BAG-family molecular chaperone regulator-3 [H.sapiens]
15172	J	169	AA859362			ESTs, Moderately similar to BAG-family molecular chaperone regulator-3 [H.sapiens]
15179	R	982	AI176675			ESTs
15181	H	1245	AI235234			ESTs
15189	M,N	1399	M11794		Metallothionein	Metallothionein
15190	N	729	AI102562		Metallothionein	Metallothionein
15191	N	964	AI176456		Metallothionein	Metallothionein
15197	A	778	AI105444			ESTs
15203	I	1389	L19698			Rat GTP-binding protein (ral A) mRNA, complete cds
15207	A,B,Q	147	AA858448			ESTs
15239	A	1619	NM_016989			R.norvegicus (Sprague Dawley) ribosomal protein L15 mRNA

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15240	A	609	AI044241			ESTs, Moderately similar to cell death activator CIDE-B [M.musculus]
15251	E,L	1011	AI177363			ESTs, Highly similar to CSK_RAT TYROSINE-PROTEIN KINASE CSK [R.norvegicus]
15281	I	1328	D13623			ESTs
15282	D,I,L	1034	AI178573			ESTs
15283	D	148	AA858548			ESTs
15291	J	780	AI111401		multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
15292	J	484	AF012714		multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
15295	O	1602	NM_013102		FK506-binding protein 1 (12kD)	FK506-binding protein 1 (12kD)
15299	A	1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15300	A,F	1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15301	A	1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15312	C,D,I,J	198	AA875126			ESTs
15313	C,D,J	198	AA875126			ESTs
15315	G	1021	AI177911		calpactin I heavy chain	calpactin I heavy chain
15345	L	902	AI171587			ESTs
15365	D	1637	NM_017147		cofilin 1, non-muscle	cofilin 1, non-muscle
15374	C,D	1368	H34186			ESTs, Highly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15382	A,J	926	AI172302			ESTs, Weakly similar to S43056 hypothetical protein - mouse [M.musculus]
15391	K	534	AI010083			Rat mRNA for HBP23 (heme-binding protein 23 kDa), complete cds
15398	C	1277	AI236566			ESTs
15433	L	1641	NM_017187		high mobility group protein 2	high mobility group protein 2
15441	K	834	AI146216			EST
15462	G	1447	U06230			Rattus norvegicus protein S mRNA, partial cds
15467	H	1265	AI236106			ESTs
15480	F	201	AA875362			ESTs
15490	J	1107	AI229253			Rattus norvegicus zinc finger protein (pMLZ-4) mRNA, 3' untranslated region
15491	H	979	AI176642			ESTs
15500	K	1110	AI229337			ESTs
15503	P	1668	NM_019237		procollagen C-proteinase enhancer protein	procollagen C-proteinase enhancer protein
15504	M,P	1668	NM_019237		procollagen C-proteinase enhancer protein	procollagen C-proteinase enhancer protein
15519	A	1036	AI178629		Proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide 7)	ESTs, Highly similar to PRCY_RAT PROTEASOME COMPONENT C13 PRECURSOR [R.norvegicus]
15534	O	955	AI176266			ESTs
15535	F	1653	NM_017283		proteasome (prosome, macropain) subunit, alpha type 6	proteasome (prosome, macropain) subunit, alpha type 6
15543	D,I	1163	AI231800			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15551	R	1138	AI230759			ESTs, Moderately similar to ornithine decarboxylase antizyme 2 [M.musculus]
15558	J	204	AA875537			ESTs
15571	G	1413	M27207		procollagen, type I, alpha 1	R.norvegicus mRNA for collagen alpha1 type I
15606	B,N	356	AA944401			ESTs
15612	A	1618	NM_016987	Citrate cycle (TCA cycle)	ATP citrate lyase	ATP citrate lyase
15616	J	1562	NM_012699		Microvascular endothelial differentiation gene 1	Microvascular endothelial differentiation gene 1
15617	J	205	AA875620			ESTs
15634	H	1546	NM_012576		Glucocorticoid receptor	Glucocorticoid receptor
15642	A	1016	AI177503			R.norvegicus mRNA for histone H3.3
15645	K	879	AI170709			R.norvegicus mRNA for histone H3.3
15647	A,J	488	AF025424	Purine metabolism, Pyrimidine metabolism	HMm:RNA polymerase 1-2 (128 kDa subunit)	Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds
15655	I,L	733	AI102739			ESTs
15663	D,R	940	AI175566			Rattus norvegicus mRNA for Tctex-1, complete cds
15672	S	281	AA900009			Rat mRNA for 5E5 antigen, complete cds
15673	G	921	AI172107			Rat mRNA for 5E5 antigen, complete cds
15700	A,D	479	AB010466			Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1), complete cds
15701	F,G	1645	NM_017220			Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-2 (MLP-2), complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15755	A,K	1718	NM_022960			Rattus norvegicus neutral solute channel aquaporin 9 (AQP9) mRNA, complete cds
15778	E	1726	NM_024163			Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds
15786	B,Q	575	AI013924			ESTs
15834	B,E	286	AA900580	Oxidative phosphorylation, Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b)	ESTs, Moderately similar to NADH-ubiquinone oxidoreductase B14.5B subunit [H.sapiens]
15860	D	738	AI102868			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15861	C,D	738	AI102868			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15862	A,C,D	1126	AI230228			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15884	A,Q	185	AA866276			ESTs
15888	K	199	AA875225			Rat guanine nucleotide-binding protein G i, alpha subunit mRNA, complete cds
15892	A,F	1074	AI179988			ESTs
15900	A,C,D	1202	AI233262			ESTs
15914	F	451	AA997711			ESTs
15933	A	200	AA875253			R.norvegicus ARL1 mRNA for ARF-like protein 1
15955	A,K,L	1175	AI232294			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15959	E,L	972	AI176540			ESTs
15961	P	550	AI012130			ESTs
15980	H	186	AA866426			ESTs
15987	K	187	AA866435			EST
16006	A,F	497	AF062594			Rattus norvegicus nucleosome assembly protein mRNA, complete cds
16023	G	225	AA891872	Nicotinate and nicotinamide metabolism	Nicotinamide nucleotide transhydrogenase (NAD(P)+ transhydrogenase)	ESTs, Highly similar to NAD(P)+ transhydrogenase [M.musculus]
16053	L	1091	AI228596			ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]
16080	A,J,Q	1547	NM_012580	Porphyrin and chlorophyll metabolism	Heme oxygenase	Heme oxygenase
16081	A,J,Q	1067	AI179610	Porphyrin and chlorophyll metabolism	Heme oxygenase	Heme oxygenase
16085	A,C,D	189	AA874889			ESTs
16087	L	1145	AI231011			ESTs
16124	K	994	AI176963			ESTs, Weakly similar to melanocyte-specific gene 1 protein [R.norvegicus]
16125	Q	503	AF090134			Rattus norvegicus lin-7-Ba mRNA, complete cds
16134	A,H	265	AA893485			Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds
16167	E	191	AA874941			ESTs, Moderately similar to adipophilin [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16169	E	598	AI030932			ESTs, Moderately similar to adipophilin [H.sapiens]
16172	A	1179	AI232341			ESTs, Weakly similar to C13B9.2 [C.elegans]
16173	M,P	408	AA957003			Rattus norvegicus intercellular calcium-binding protein (MRP8) mRNA, complete cds
16190	A,S	757	AI104482			ESTs, Weakly similar to ECHM_RAT ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR [R.norvegicus]
16205	L	1488	X06423			Rat mRNA for ribosomal protein S8
16215	H	192	AA874999			ESTs, Moderately similar to AF133910_1 ARL-6 interacting protein-3 [M.musculus]
16219	G	1557	NM_012656		Secreted acidic cystein-rich glycoprotein (osteonectin)	Secreted acidic cystein-rich glycoprotein (osteonectin)
16240	M	166	AA859342			ESTs, Moderately similar to DHB2_RAT ESTRADIOL 17 BETA-DEHYDROGENASE 2 [R.norvegicus]
16251	E,Q	347	AA944077		Solute carrier family 2 a 1 (facilitated glucose transporter) brain	Rat brain glucose-transporter protein mRNA, complete cds
16278	E,K	1338	D38381	Fatty acid metabolism, Tryptophan metabolism	Hsp:CYTOCHROME P450 3A18	R.norvegicus CYP3 mRNA
16283	O	1667	NM_019229		solute carrier family 12, member 4	solute carrier family 12, member 4
16312	A	193	AA875032			ESTs
16314	A	167	AA859348			ESTs
16317	B	194	AA875041			ESTs, Moderately similar to AF123655_1 FEZ1 [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16318	J	174	AA859648			ESTs, Weakly similar to DnaJ homolog 2 [R.norvegicus]
16319	K	195	AA875047			ESTs, Highly similar to TCPZ_MOUSE T COMPLEX PROTEIN 1, ZETA SUBUNIT [M.musculus]
16321	C	1157	AI231506			ESTs
16323	S	184	AA866240			EST
16324	A	722	AI102009			ESTs
16327	A,O	196	AA875050			ESTs, Weakly similar to choline/ethanolamine kinase [R.norvegicus]
16361	H	1442	U01344		Hsp:ARYLAMINE N-ACETYLTRANSFERASE 1	Rattus norvegicus clone A-2 arylamine N acetyltransferase mRNA, complete cds
16364	A,H	235	AA892251			R.norvegicus mRNA for V1a arginine vasopressin receptor
16366	P	250	AA892888			EST
16367	P	250	AA892888			EST
16408	F	145	AA852027			ESTs
16409	S	145	AA852027			ESTs
16438	I	958	AI176294			ESTs, Highly similar to SMD2_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2 [H.sapiens]
16446	A	214	AA891423			ESTs
16449	H	1669	NM_019238	Sterol biosynthesis	farnesyl diphosphate farnesyl transferase 1	farnesyl diphosphate farnesyl transferase 1
16458	B,Q	362	AA944956			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16477	Q	983	AI176701			Rat low molecular weight fatty acid binding protein mRNA, complete cds
16513	C	118	AA848782			ESTs, Moderately similar to hypothetical protein [M.musculus]
16518	D	973	AI176546			ESTs, Weakly similar to HS9B_RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
16519	P	1539	NM_012532	Porphyrin and chlorophyll metabolism	Ceruloplasmin (ferroxidase)	Ceruloplasmin (ferroxidase)
16524	H	1362	H33219			ESTs
16562	E,N	904	AI171630			Rattus norvegicus p38 mitogen activated protein kinase mRNA, complete cds
16566	H	1131	AI230395			Rattus norvegicus mRNA for TIP120, complete cds
16610	I	1333	D28557			Rattus norvegicus muscle Y-box protein YB2 mRNA, complete cds
16616	R	1230	AI234079			ESTs
16618	C	837	AI168967			ESTs
16623	E	1150	AI231196			ESTs
16649	I	1606	NM_013132		Annexin V	Annexin V
16650	I	1606	NM_013132		Annexin V	Annexin V
16654	I	1522	X98517			R.norvegicus mRNA for macrophage *metalloelastase* (MME)
16673	R	759	AI104608			ESTs
16680	A	436	AA965190			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16683	I	1596	NM_013052		Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
16684	I,O	1596	NM_013052		Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
16688	L	870	AI170327			ESTs
16700	A,E,S	517	AI008838			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16701	A	517	AI008838			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16703	A,C,O	1060	AI179300			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16704	S	4	AA686132			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16726	A	1427	M86235	Fructose and mannose metabolism	Hsp:KETOHEXOKINASE	Rat ketohexokinase mRNA, complete cds
16728	H	1020	AI177885			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16730	A,I	23	AA799766			ESTs, Moderately similar to JTV1_HUMAN JTV-1 PROTEIN [H.sapiens]
16747	L	336	AA943131			ESTs
16756	C,D	52	AA818089			ESTs, Highly similar to glycyl-tRNA synthetase [H.sapiens]
16765	A	632	AI058319			ESTs
16766	A	682	AI072137			ESTs
16768	N	1331	D16478	Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Rat mRNA for mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of mitochondrial trifunctional protein, complete cds
16780	E,K	1510	X62660			ESTs, Highly similar to glutathione transferase [R.norvegicus]
16783	L,O	553	AI012215			ESTs, Weakly similar to nonmuscle myosin heavy chain-A [R.norvegicus]
16809	B,O,Q	1503	X58828		Hsp:PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2	Rat PTP-S mRNA for protein-tyrosine phosphatase
16825	J	245	AA892602			ESTs
16854	I	188	AA866454			Rat alpha-2(I) promoter
16859	A,C,N	1283	AI236753			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16871	H	1583	NM_012887		Thymopoietin (lamina associated polypeptide 2)	Thymopoietin (lamina associated polypeptide 2)
16879	A,E,F	848	AI169284			ESTs
16883	A,C,D,I	446	AA997345			ESTs, Weakly similar to nitrilase homolog 1 [M.musculus]
16884	B,E	754	AI103758	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism	HHs:aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	Rattus norvegicus 4-trimethylaminobutyraldehyde dehydrogenase (Tmabadh) mRNA, complete cds
16885	A,B,E,Q	773	AI105188	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism	HHs:aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	Rattus norvegicus 4-trimethylaminobutyraldehyde dehydrogenase (Tmabadh) mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16894	O	144	AA852018			ESTs, Moderately similar to AF097362_1 gamma-interferon inducible lysosomal thiol reductase [H.sapiens]
16944	S	320	AA925541			ESTs, Highly similar to protein L [M.musculus]
16945	S	320	AA925541			ESTs, Highly similar to protein L [M.musculus]
16947	E	1572	NM_012793	Arginine and proline metabolism,Glycine, serine and threonine metabolism,Urea cycle and metabolism of amino groups	Guanidinoacetate methyltransferase	Guanidinoacetate methyltransferase
16958	G	92	AA819021			EST
16961	P	1058	AI179236			ESTs
16982	A	1608	NM_013144		Insulin-like growth factor binding protein 1	Insulin-like growth factor binding protein 1
16993	A	14	AA799560			ESTs
17027	A,E	877	AI170679	Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism	HHs:UDP-glucose pyrophosphorylase 2	ESTs, Highly similar to UDP1_HUMAN UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE 1 [H.sapiens]
17049	A	929	AI172417			ESTs, Weakly similar to Similarity to B.subtilis YQJC protein [C.elegans]
17064	I	1660	NM_019170	Prostaglandin and leukotriene metabolism	carbonyl reductase	carbonyl reductase

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17090	G,K	1474	U73174	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17091	G,K	1474	U73174	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17092	K	259	AA893189	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17107	E	1638	NM_017160		ribosomal protein S6	ribosomal protein S6
17117	K	1085	AI228042			ESTs, Weakly similar to AC007080_2 NG38 [M.musculus]
17154	A	1407	M15883			Rat clathrin light chain (LCB2) mRNA, complete cds,Rat clathrin light chain (LCB3) mRNA, complete cds
17157	I	326	AA926129			ESTs, Highly similar to AF168795_1 schlafen-4 [R.norvegicus]
17158	H	1699	NM_022298			Rat mRNA encoding alpha-tubulin
17167	M	566	AI013690			ESTs
17175	A	1501	X58389			R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
17225	A,I	215	AA891553			ESTs, Highly similar to eIF3 p66 [M.musculus]
17256	A	219	AA891739			ESTs, Weakly similar to p60 protein [R.norvegicus]
17257	E,R	1568	NM_012766		Cyclin D3	Cyclin D3
17258	P	1568	NM_012766		Cyclin D3	Cyclin D3
17261	R	1568	NM_012766		Cyclin D3	Cyclin D3
17277	B,P,Q	523	AI009338			Rattus norvegicus glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17281	M,P	1450	U10697		Hsp:LIVER CARBOXYLESTERASE 4 PRECURSOR	R.norvegicus mRNA for pI esterase (ES-4)
17291	E	931	AI172491	Citrate cycle (TCA cycle), Glutathione metabolism	HHs:isocitrate dehydrogenase 2 (NADP+), mitochondrial	ESTs, Weakly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE [R.norvegicus]
17324	A	1686	NM_021593			Rattus norvegicus kynurenine 3-hydroxylase mRNA, complete cds
17334	A	151	AA858704			ESTs, Highly similar to responsible for hereditary multiple exotosis [M.musculus]
17335	A	732	AI102634			ESTs, Weakly similar to W06B4.2 [C.elegans]
17337	J	472	AB000717	Methionine metabolism, Selenoamino acid metabolism	HHs:methionine adenosyltransferase II, alpha	ESTs
17339	A	123	AA849497			ESTs
17340	A,E	507	AI007803			Rattus norvegicus ERM-binding phosphoprotein mRNA, complete cds
17368	E,R	284	AA900548			ESTs
17369	C,I,P	812	AI137572			ESTs
17377	A	1491	X13058		Tumor protein p53 (Li-Fraumeni syndrome)	Rat mRNA for nuclear oncoprotein p53
17393	A,O	1377	J04943		Nucleoplasmin-related protein (Nuclear protein B23	Nucleoplasmin-related protein (Nuclear protein B23
17400	E	744	AI103097			ESTs, Highly similar to ATPK_MOUSE ATP SYNTHASE F CHAIN, MITOCHONDRIAL [M.musculus]
17401	A	1595	NM_013043		Transforming growth factor beta stimulated clone 22	Transforming growth factor beta stimulated clone 22

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17451	E	806	AI137356			ESTs, Highly similar to DHYS_HUMAN DEOXYHYPUSINE SYNTHASE [H.sapiens]
17479	R	827	AI145385			ESTs
17481	E	1529	Z49761			R.norvegicus mRNA for RT1.Ma
17496	A	325	AA926109			ESTs
17500	I,P	1713	NM_022866			Rattus norvegicus sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
17506	L	649	AI070068			ESTs
17516	O	1739	NM_017321		iron-responsive element-binding protein	iron-responsive element-binding protein
17524	A	539	AI010568			ESTs
17541	G,K	1580	NM_012844		Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)
17571	H,I	1276	AI236484			Rattus norvegicus mRNA for hnRNP protein, partial
17572	E	71	AA818524			Rattus norvegicus mRNA for hnRNP protein, partial
17589	A	248	AA892851			ESTs
17590	F	248	AA892851			ESTs
17591	A	898	AI171354			ESTs
17613	O	10	AA799511			ESTs
17617	E	1269	AI236301			ESTs, Weakly similar to FKB1_RAT FK506-BINDING PROTEIN [R.norvegicus]
17644	R	293	AA924036			ESTs
17664	B,Q	1238	AI234496			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17672	N	1123	AI230074	Oxidative phosphorylation, Ubiquinone biosynthesis	HMm:NADH ubiquinone oxidoreductase subunit MWFE	ESTs, Highly similar to NIMM_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT [M.musculus]
17677	E	683	AI072246			ESTs
17683	N	700	AI073257			ESTs
17684	G	236	AA892345			Rat mRNA for dimethylglycine dehydrogenase (EC number 1.5.99.2)
17685	K	797	AI113055			EST
17687	C	12	AA799531			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
17688	A	12	AA799531			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
17695	N	1192	AI232784			ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]
17699	O	135	AA851233			ESTs, Weakly similar to NG28 [M.musculus]
17709	A	1456	U24489		Tenascin X	Tenascin X
17730	G	1709	NM_022697			Rat mRNA for ribosomal protein L28
17734	C,D	466	AA998683			ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds
17735	C,D,J	981	AI176658			ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds
17736	C,D	1428	M86389			ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds
17747	E	1236	AI234223			ESTs, Highly similar to cellular apoptosis susceptibility protein [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17753	J	748	AI103246			ESTs, Highly similar to S65568 CCAAT-binding factor CBF2 - mouse [M.musculus]
17754	I	261	AA893246			ESTs, Highly similar to vacuolar H-ATPase subunit D [H.sapiens]
17758	G	1645	NM_017220	Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism	HHs:enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Rat peroxisomal enoyl-CoA: hydrotase-3 hydroxyacyl-CoA bifunctional enzyme mRNA, complete cds
17768	B	774	AI105196			ESTs
17785	N	1534	NM_012501		Apolipoprotein C-III	Apolipoprotein C-III
17788	K	271	AA899045		Esterase D/formylglutathione hydrolase	ESTs, Highly similar to sid478p [M.musculus]
17794	E,N	772	AI105184	Cyanoamino acid metabolism,Glycine, serine and threonine metabolism,Lysine degradation,Methane metabolism,One carbon pool by folate	HHs:serine hydroxymethyltransferase 1 (soluble)	ESTs
17800	N	262	AA893436			ESTs
17809	B	5	AA686461			Rat ribosomal protein L30 mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17812	A,E	841	AI169075	Glutathione metabolism, Tyrosine metabolism	HMm:glutathione transferase zeta 1 (maleylacetoacetate isomerase)	ESTs
17819	A	891	AI171095			ESTs, Highly similar to unknown [H.sapiens]
17844	A,E	398	AA955927			ESTs
17847	A	1025	AI178214			ESTs
17850	A	734	AI102750			ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
17854	Q	1490	X13016			Rat mRNA for MRC OX-45 surface antigen
17894	E,F	1594	NM_013027		Selenoprotein W muscle 1	Selenoprotein W muscle 1
17908	A,J	1670	NM_019242		interferon-related developmental regulator 1	interferon-related developmental regulator 1
17935	S	289	AA901006			Rattus norvegicus membrane interacting protein of RGS16 (Mir16) mRNA, complete cds
17950	Q	1278	AI236590		myeloid differentiation primary response gene 88	ESTs
17955	L	590	AI030069			ESTs
17956	I	427	AA964379		adaptor-related protein complex AP-1, beta 1 subunit	adaptor-related protein complex AP-1, beta 1 subunit
17982	A	1727	NM_017010		Glutamate receptor, ionotropic, N-methyl D-aspartate 1	Glutamate receptor, ionotropic, N-methyl D-aspartate 1,Rat N-methyl-D-aspartate receptor (NMDAR1) gene, first exon

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18001	A	149	AA858573			ESTs, Highly similar to SP24_RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus],Rattus norvegicus spp-24 precursor mRNA, partial cds
18002	A,D,E	600	AI043655			ESTs, Highly similar to SP24_RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus],Rattus norvegicus spp-24 precursor mRNA, partial cds
18028	G	1337	D38062			Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds
18029	S	1418	M38759		Sex hormone binding globulin or androgen-binding protein	Sex hormone binding globulin or androgen-binding protein
18043	J	487	AF020618			Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds
18046	I	500	AF072892			Rattus norvegicus versican V0 isoform mRNA, partial cds,Rattus norvegicus versican V3 isoform precursor, mRNA, complete cds
18082	S	478	AB010429			R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase
18083	S	1524	Y09333		Hsp:ACYL COENZYME A THIOESTER HYDROLASE, MITOCHONDRIAL PRECURSOR	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase
18099	G	1604	NM_013119			ESTs, Highly similar to A60054 sodium channel protein IIIb, long form - rat [R.norvegicus]
18107	I	1717	NM_022949			R.norvegicus mRNA for ribosomal protein L14

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18109	A	1577	NM_012823		Annexin III (Lipocortin III)	ESTs, Weakly similar to LURT3 annexin III - rat [R.norvegicus]
18115	A	31	AA800339			ESTs
18125	S	515	AI008787			ESTs
18136	H	737	AI102820			ESTs
18141	O	1014	AI177413		ATP synthase subunit d	ATP synthase subunit d,ESTs, Weakly similar to myo-inositol-1-phosphate synthase [D.melanogaster]
18203	P	1584	NM_012891			ESTs, Highly similar to ACDV_RAT ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR [R.norvegicus]
18235	L	758	AI104523			ESTs
18237	Q	1065	AI179539			ESTs, Highly similar to CDC45L [M.musculus]
18259	J	1280	AI236601			ESTs
18272	B	6	AA799294			ESTs, Moderately similar to KIAA0740 protein [H.sapiens]
18280	L	384	AA946361			ESTs, Highly similar to Ring3 [M.musculus]
18285	R	341	AA943791			ESTs
18316	K	499	AF072411			Rattus norvegicus FAT mRNA, complete cds
18318	S	385	AA946368			Rattus norvegicus FAT mRNA, complete cds
18323	E	556	AI012498			ESTs
18349	J	22	AA799744			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18369	G	19	AA799645			Rattus norvegicus phospholemman chloride channel mRNA, complete cds
18389	A,B,Q	9	AA799498		Brain natriuretic factor	Rattus norvegicus brain natriuretic peptide (BNP) mRNA, complete cds
18390	A,E	128	AA850038			ESTs
18418	C	969	AI176483			ESTs
18452	A	1630	NM_017074	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism	CTL target antigen	CTL target antigen
18453	A	1630	NM_017074	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism	CTL target antigen	CTL target antigen
18465	B,Q	1077	AI180187			ESTs
18473	K	838	AI168975			ESTs
18482	H	1311	AI639151			ESTs, Highly similar to pinin [H.sapiens]
18484	L	1249	AI235349			ESTs, Highly similar to KIAA0184 [H.sapiens]
18495	B	1307	AI639042			ESTs
18501	J	1414	M31178			Rat calbindin D28 mRNA, complete cds
18522	A,E	830	AI145870			ESTs
18529	B,Q	1136	AI230716			ESTs
18580	M,P	142	AA851963			ESTs
18584	H	216	AA891694			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18588	E	276	AA899635			ESTs, Moderately similar to 2020285A BRG1 protein [M.musculus]
18597	A	481	AB013732	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism	HMm:UDP-glucose dehydrogenase	Rattus norvegicus mRNA for UDP-glucose dehydrogeanse, complete cds
18604	N	1292	AI237124			ESTs
18606	A	1497	X53504			ESTs, Highly similar to RL12_RAT 60S RIBOSOMAL PROTEIN L12 [R.norvegicus]
18612	E,O	1092	AI228624			ESTs, Highly similar to RL23_HUMAN 60S RIBOSOMAL PROTEIN L23 [R.norvegicus]
18647	E	1435	S69316			ESTs, Weakly similar to HS9B_RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
18660	A	894	AI171262		cyclin G2	ESTs
18661	A	376	AA945751			ESTs
18685	L	453	AA997746	Fatty acid metabolism	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)
18705	I	1732	NM_020103		Ly6-C antigen gene	Ly6-C antigen gene
18727	S	1685	NM_021577	Alanine and aspartate metabolism,Arginine and proline metabolism,Urea cycle and metabolism of amino groups	HHs:argininosuccinate lyase	Rat mRNA for argininosuccinate lyase, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18742	O,S	769	AI105131			ESTs, Highly similar to AF189764_1 alpha/beta hydrolase-1 [M.musculus]
18746	S	900	AI171506	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
18747	S	1550	NM_012600	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
18749	S	1550	NM_012600	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
18755	C,D	1279	AI236599			ESTs
18783	N	1282	AI236746			ESTs
18792	A	662	AI071177			ESTs
18795	N	1483	U95001			ESTs
18796	A	45	AA817761			ESTs
18829	H	84	AA818796			ESTs
18837	G	901	AI171583			ESTs, Moderately similar to PLTP_MOUSE PHOSPHOLIPID TRANSFER PROTEIN PRECURSOR [M.musculus]
18854	A	1300	AI237636			ESTs, Weakly similar to N-copine [M.musculus]
18860	A,K	861	AI169695			Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
18861	A	1329	D14989	Androgen and estrogen metabolism,Sulfur metabolism	Hsp:ALCOHOL SULFOTRANSFERASE	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
18867	A	1348	D88250			Rattus norvegicus mRNA for serine protease, complete cds
18877	O	686	AI072393			ESTs
18885	R	583	AI029827			ESTs, Highly similar to AF157028_1 protein phosphatase methylesterase-1 [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18886	R	340	AA943785			ESTs,ESTs, Highly similar to AF157028_1 protein phosphatase methylesterase-1 [H.sapiens]
18890	B,P,S	280	AA899964			ESTs
18891	B,Q,S	303	AA924598			ESTs
18900	F	1214	AI233570			ESTs, Highly similar to PSD8_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 [H.sapiens]
18905	E	883	AI170770	Oxidative phosphorylation,Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NADH-ubiquinone oxidoreductase NDUFS2 subunit [H.sapiens]
18906	A,K	243	AA892561			ESTs, Moderately similar to PTD012 [H.sapiens]
18908	A	122	AA849426			ESTs
18909	A	122	AA849426			ESTs
18910	A	1182	AI232419			ESTs
18956	S	1631	NM_017075	Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies, Tryptophan metabolism	Acetyl-Co A acetyltransferase 1, mitochondrial	Acetyl-Co A acetyltransferase 1, mitochondrial
18960	A	1004	AI177103			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18962	R	574	AI013918			Rattus norvegicus TM6P1 (TM6P1) mRNA, complete cds
18974	M	319	AA925384			EST
18981	H	11	AA799523			ESTs, Moderately similar to hnRNP protein [R.norvegicus]
18990	G	1438	S72506	Glutathione metabolism	Glutathione-S-transferase, alpha type (Yc?)	Glutathione-S-transferase, alpha type (Yc?)
18996	N	1027	AI178326			ESTs
19012	J,K	918	AI172056			ESTs
19040	I	1374	J03627			Rat S-100 related protein mRNA, complete cds, clone 42C
19043	F	130	AA850378			ESTs, Highly similar to methyl-CpG binding protein MBD2 [M.musculus]
19044	S	386	AA946379			ESTs, Highly similar to methyl-CpG binding protein MBD2 [M.musculus]
19052	E,R	1253	AI235675			ESTs
19053	K	1327	D12770			Rattus norvegicus mRNA for mitochondrial adenine nucleotide translocator
19069	A,L	339	AA943737			ESTs
19073	F	34	AA800576			ESTs
19075	B,J	1275	AI236473			ESTs, Moderately similar to cysteine-rich hydrophobic 1 [M.musculus]
19085	A,J	244	AA892598			ESTs
19086	A,J	244	AA892598			ESTs
19103	A	36	AA800797			ESTs
19105	E	162	AA859230			ESTs, Highly similar to HG14_MOUSE NONHISTONE CHROMOSOMAL PROTEIN HMG-14 [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19121	P	608	AI044101			ESTs
19150	C	8	AA799461			ESTs
19158	B	140	AA851953			ESTs, Moderately similar to hypothetical protein [H.sapiens]
19184	J	1022	AI178025			ESTs, Highly similar to TGIF_MOUSE 5'-TG-3' INTERACTING FACTOR [M.musculus]
19211	N	136	AA851329			ESTs
19230	R	646	AI059604			ESTs
19241	I	1666	NM_019206		Serine/threonine kinase 10	Serine/threonine kinase 10
19252	N		NM_019382		anti-oxidant protein 2	anti-oxidant protein 2
19255	K	1406	M15562			Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
19256	K	1406	M15562			Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
19258	O	287	AA900613			ESTs
19261	O	741	AI102943			ESTs
19264	C,D,R	743	AI103078			ESTs
19292	K	445	AA997323			EST
19298	A,D,I	1272	AI236338			ESTs, Weakly similar to NHPX_RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus]
19315	E	1144	AI231010			EST
19363	A,F	954	AI176247			ESTs, Moderately similar to unnamed protein product [H.sapiens]
19373	N	1684	NM_021266		Hyaluronan mediated motility receptor (RHAMM)	Hyaluronan mediated motility receptor (RHAMM)

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19377	I	180	AA859971			ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
19388	F	206	AA891032			EST
19392	M	1592	NM_012998	Arginine and proline metabolism,Biosynthesis and degradation of glycoprotein	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
19410	B,Q	268	AA893667			ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19411	M,P	268	AA893667			ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19412	B,Q	120	AA849222			ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19444	P	309	AA924993			ESTs
19458	E	462	AA998345			EST
19465	K	630	AI045881			EST
19469	A,P	231	AA892112			ESTs, Weakly similar to proline dehydrogenase [M.musculus]
19470	A	1203	AI233266			ESTs, Weakly similar to proline dehydrogenase [M.musculus]
19476	O	1188	AI232612			ESTs
19503	P	116	AA848639			ESTs, Moderately similar to vascular endothelial growth factor D [M.musculus]
19508	A	1114	AI229698			EST

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19512	M	855	AI169612			Rattus norvegicus adipocyte lipid-binding protein (ALBP) mRNA, complete cds
19513	R	1100	AI229035			ESTs
19566	E	112	AA819879			ESTs, Highly similar to ATP binding protein [H.sapiens]
19591	S	559	AI012747			ESTs
19605	E,L	97	AA819172			EST
19641	J	663	AI071181			EST
19650	H	486	AF016387			ESTs,Rattus norvegicus retinoid X receptor gamma (RXRgamma) mRNA, partial cds
19669	R	1740	NM_022944			Rattus norvegicus mRNA for SH2-containing inositol phosphatase 2 (SHIP2), complete cds
19671	B,Q	1656	NM_017309		protein phospatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	protein phospatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)
19678	A	1733	NM_021653		Thyroxine deiodinase, type I	Rat mRNA for type I thyroxine deiodinase
19679	A	1733	NM_021653		Thyroxine deiodinase, type I	Rat mRNA for type I thyroxine deiodinase
19715	M	1662	NM_019190		membrane cofactor protein	membrane cofactor protein
19728	O	872	AI170394			ESTs
19729	A	87	AA818910			ESTs
19732	A,G	1262	AI236066			ESTs
19762	R	272	AA899113			EST
19768	I	237	AA892373			ESTs
19787	H	1304	AI638994			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19824	O	1688	NM_021750	Taurine and hypotaurine metabolism	HHs:cysteine sulfinic acid decarboxylase-relatedprotein 2	Rattus norvegicus brain mRNA for cysteine-sulfinate decarboxylase
19825	O	1688	NM_021750	Taurine and hypotaurine metabolism	HHs:cysteine sulfinic acid decarboxylase-relatedprotein 2	Rattus norvegicus brain mRNA for cysteine-sulfinate decarboxylase
19830	A	853	AI169529			ESTs, Weakly similar to 3O5B_RAT 3-OXO-5-BETA-STEROID 4-DEHYDROGENASE [R.norvegicus]
19843	A	1308	AI639055			EST
19909	A	1315	AI639310			EST
19940	C	1254	AI235689			ESTs, Moderately similar to pescadillo [H.sapiens]
19952	A	1310	AI639108			ESTs
20016	B	1312	AI639158			ESTs, Moderately similar to dJ967N21.3 [H.sapiens]
20035	A	1689	NM_021754			Rattus norvegicus Nopp140 associated protein (NAP65) mRNA, complete cds
20038	S	278	AA899797			EST
20041	K	787	AI112161			ESTs
20063	E,L	313	AA925063			ESTs, Highly similar to R32184_3 [H.sapiens]
20082	C	1316	AI639488			EST, Highly similar to A42772 mdm2 protein - rat [R.norvegicus]
20088	A	246	AA892666			ESTs
20090	R	1690	NM_021757			Rattus norvegicus pleiotropic regulator 1 (PLRG1) mRNA, complete cds
20119	P	1033	AI178533			EST, Moderately similar to TNFC_MOUSE LYMPHOTOXIN-BETA [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20134	P	1692	NM_021852			Rattus norvegicus EH domain binding protein epsin 2 mRNA, complete cds
20161	A,B	1691	NM_021836			R.norvegicus pJunB gene
20200	M	1693	NM_022194			Rat interleukin 1 receptor antagonist gene, complete cds
20282	H	1648	NM_017274	Glycerolipid metabolism	glycerol-3-phosphate acyltransferase, mitochondrial	glycerol-3-phosphate acyltransferase, mitochondrial
20299	A,D	1694	NM_022220			Rattus norvegicus gene for L-gulono-gamma-lactone oxidase
20350	L,Q	1186	AI232552			EST
20354	B,N,Q	1404	M14369		K-kininogen, differential splicing leads to HMW Kngk	K-kininogen, differential splicing leads to HMW Kngk
20380	E,G	1330	D16102	Glycerolipid metabolism	glycerol kinase	*Rattus norvegicus* mRNA for ATP-stimulated glucocorticoid-receptor translocaton promoter, complete cds
20397	A,E	1151	AI231226			ESTs, Moderately similar to SYM_HUMAN METHIONYL-TRNA SYNTHETASE [H.sapiens]
20449	A,C,I	1494	X17053		Small inducible gene JE	Rattus norvegicus JE/MCP-1 mRNA, complete cds
20456	A,C	1355	H31144			ESTs
20502	A,F	370	AA945533			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)
20503	A,C,E	864	AI169779			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20513	A	1554	NM_012624	Glycolysis/ Gluconeogenesis, Purine metabolism, Pyruvate metabolism	Pyruvate kinase, liver and RBC	Pyruvate kinase, liver and RBC
20522	P	224	AA891842			ESTs, Moderately similar to podocalyxin [R.norvegicus]
20523	C,P	224	AA891842			ESTs, Moderately similar to podocalyxin [R.norvegicus]
20529	F,M,P	1644	NM_017208		lipopolysaccharide binding protein	lipopolysaccharide binding protein
20555	G	1458	U26033			Rattus norvegicus carnitine octanoyltransferase mRNA, complete cds
20579	O	1654	NM_017288		sodium channel, voltage-gated, type I, beta polypeptide	sodium channel, voltage-gated, type I, beta polypeptide
20589	I	1553	NM_012618		Protein 9 Ka homologous to calcium-binding protein	Protein 9 Ka homologous to calcium-binding protein
20597	S	1489	X12459	Alanine and aspartate metabolism,Arginine and proline metabolism,Urea cycle and metabolism of amino groups	Arginosuccinate synthetase 1	Arginosuccinate synthetase 1
20644	I	996	AI176990			ESTs, Highly similar to SRPR_HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT [H.sapiens]
20651	P	1460	U36992		Cytochrom P450	Cytochrom P450
20684	C	1361	H32977			ESTs
20694	A	442	AA997048			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20698	N	1519	X86561			Rat alpha-fibrinogen mRNA, 3' end
20701	A,B,F,Q	197	AA875097			Rat alpha-fibrinogen mRNA, 3' end
20705	A,D	1541	NM_012541	Fatty acid metabolism,Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
20707	A,D,K	1481	U88036			Rattus norvegicus brain digoxin carrier protein mRNA, complete cds
20708	C,F	476	AB006461			Rattus norvegicus mRNA for NORBIN, complete cds
20711	E,K	1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20713	K	1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20714	K	1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20715	E,N	1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20734	A	1672	NM_019283		antigen identified by monoclonal antibodies 4F2	antigen identified by monoclonal antibodies 4F2
20735	A,C,D	1672	NM_019283		antigen identified by monoclonal antibodies 4F2	antigen identified by monoclonal antibodies 4F2
20741	F	502	AF084186			R.norvegicus mRNA for alpha II spectrin

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20744	K	1545	NM_012571	Alanine and aspartate metabolism, Arginine and proline metabolism, Cysteine metabolism, Glutamate metabolism, Phenylalanine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12
20755	I	1587	NM_012923		Cyclin G1	Cyclin G1
20757	A	1587	NM_012923		Cyclin G1	Cyclin G1
20772	A,F	1468	U60882			Rattus norvegicus protein arginine N-methyltransferase (PRMT1) mRNA, complete cds
20795	J	355	AA944397			ESTs, Moderately similar to HS9B_RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
20799	H	1405	M15428	egf,epo,il2,il3,il6,insulin,interact6-1,ngf,pdgf,tpo	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)
20801	A,I	1723	NM_024148		Apurinic/apyrimidinic endonuclease 1	Rattus norvegicus mRNA for APEX nuclease, complete cds
20803	K	1707	NM_022592	Pentose phosphate cycle	HMm:transketolase	Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds
20804	K	1707	NM_022592	Pentose phosphate cycle	HMm:transketolase	Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds
20810	A	1493	X14181			ESTs, Highly similar to RL1X_RAT 60S RIBOSOMAL PROTEIN L18A [R.norvegicus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20817	G	558	AI012589	Glutathione metabolism	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2
20818	G	1485	X02904	Glutathione metabolism	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2
20843	C,D	13	AA799545			ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
20846	E,N	1147	AI231140			ESTs, Highly similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [R.norvegicus]
20849	F,I	1487	X05566			Rat mRNA for myosin regulatory light chain (RLC)
20851	E	1614	NM_013214		acyl-CoA hydrolase	acyl-CoA hydrolase
20855	S	1613	NM_013200	Fatty acid metabolism, Glycerolipid metabolism	Carnitine palmitoyltransferase 1 beta, muscle isoform	Carnitine palmitoyltransferase 1 beta, muscle isoform
20856	S	1613	NM_013200	Fatty acid metabolism, Glycerolipid metabolism	Carnitine palmitoyltransferase 1 beta, muscle isoform	Carnitine palmitoyltransferase 1 beta, muscle isoform
20864	G,K,P	1615	NM_013215		aflatoxin B1 aldehyde reductase	aflatoxin B1 aldehyde reductase
20873	G	1000	AI177042			ESTs, Highly similar to RS19_RAT 40S RIBOSOMAL PROTEIN S19 [R.norvegicus]
20874	A	1116	AI229789			ESTs, Moderately similar to KIAA0952 protein [H.sapiens]
20879	I	1511	X65296			R.norvegicus mRNA for pI 6.1 esterase (ES-10)
20889	A	1563	NM_012716		Solute carrier 16 (monocarboxylic acid transporter), member 1	Solute carrier 16 (monocarboxylic acid transporter), member 1
20891	A,C,I	852	AI169337			ESTs, Highly similar to CGI-117 protein [H.sapiens]
20897	I	945	AI175812			ESTs, Highly similar to Copa protein [M.musculus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20914	B	1412	M23995		Aldehyde dehydrogenase 1 (phenobarbitol inducible)	Aldehyde dehydrogenase 1 (phenobarbitol inducible)
20915	K,Q	1730	NM_017272		Aldehyde dehydrogenase 1 (phenobarbitol inducible)	Aldehyde dehydrogenase 1 (phenobarbitol inducible)
20930	E	473	AB004096	Fatty acid metabolism, Tryptophan metabolism	Cytochrom P450 Lanosterol 14 alpha-demethylase	Cytochrom P450 Lanosterol 14 alpha-demethylase
20950	I	7	AA799323			ESTs, Moderately similar to PLEK_HUMAN PLECKSTRIN [H.sapiens]
20971	H	15	AA799576			ESTs, Weakly similar to nucleolar RNA helicase II/Gu [M.musculus]
20975	H	16	AA799599			ESTs
20980	E	18	AA799633			ESTs
20983	F	619	AI044900		Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain
20986	G	260	AA893242		Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain
20993	R	1041	AI178741			ESTs
20998	S	24	AA799803			ESTs, Weakly similar to serine protease [R.norvegicus]
21010	S	318	AA925306	Alanine and aspartate metabolism	HMm:carnitine acetyltransferase	ESTs
21014	P	1376	J03914	Glutathione metabolism	Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
21025	A	163	AA859241		synaptojanin 2 binding protein	Rattus norvegicus NPW16 mRNA, complete cds
21039	B	1373	J03190	Glycine, serine and threonine metabolism	HHs:aminolevulinate, delta-, synthase 1	Rat 5-aminolevulinate synthase mRNA, complete cds
21040	E	546	AI011734	Glycine, serine and threonine metabolism	HHs:aminolevulinate, delta-, synthase 1	Rat 5-aminolevulinate synthase mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21060	I	547	AI011746			ESTs, Weakly similar to BACR7C10.a [D.melanogaster]
21068	E	943	AI175675			ESTs, Highly similar to RB24_MOUSE RAS-RELATED PROTEIN RAB-24 [M.musculus]
21075	P	1706	NM_022584		thioredoxin reductase 2	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds
21078	K	1617	NM_016986	Fatty acid metabolism, Propanoate metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain
21088	A,F	966	AI176472			ESTs
21091	E	1289	AI236972			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
21097	A,H,N	1400	M12112		Angiotensinogen	Rat angiotensinogen (PAT) gene
21098	N	344	AA943892		Angiotensinogen	Rat angiotensinogen (PAT) gene
21125	A	114	AA848437			ESTs
21130	J	959	AI176298			ESTs
21150	A	119	AA848826			ESTs
21157	A	383	AA946189			ESTs
21164	O,S	810	AI137488			ESTs
21175	H	768	AI105113			ESTs
21184	K	709	AI101205			ESTs
21209	A,E	913	AI171772			ESTs
21228	K,M	615	AI044404			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21238	K	1719	NM_024125	il6,interact6-1	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)	Rat sfb mRNA for silencer factor B
21256	Q	1029	AI178491			ESTs
21275	L	125	AA849796			ESTs
21281	B,E,M	1231	AI234090			ESTs, Moderately similar to hypothetical protein [H.sapiens]
21285	P	126	AA849898			EST
21305	G	258	AA893082			ESTs
21321	H	1227	AI233902			ESTs
21341	A,S	129	AA850195			ESTs
21354	S	277	AA899721			ESTs
21380	J	35	AA800739			ESTs, Weakly similar to /prediction
21382	N	375	AA945708			ESTs
21396	A	1612	NM_013198	Arginine and proline metabolism,Glycine, serine and threonine metabolism,Histidine metabolism,Phenylalanine metabolism,Tryptophan metabolism,Tyrosine metabolism	Monoamine oxidase B	Monoamine oxidase B
21414	P	1255	AI235842			ESTs
21416	I	37	AA800962			ESTs, Highly similar to TALI_MOUSE TALIN [M.musculus]
21421	N	1664	NM_019196		multiple PDZ domain protein	multiple PDZ domain protein
21443	P,Q	1671	NM_019262		complement component 1, q subcomponent, beta polypeptide	complement component 1, q subcomponent, beta polypeptide

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21444	Q	1671	NM_019262		complement component 1, q subcomponent, beta polypeptide	complement component 1, q subcomponent, beta polypeptide
21445	M,P	1388	L18948			Rattus norvegicus intracellular calcium-binding protein (MRP14) mRNA, complete cds
21458	C	311	AA925049			ESTs
21467	N	951	AI176061			ESTs; Weakly similar to tazarotene-induced gene 2 [H.sapiens]
21471	A	137	AA851343			ESTs
21535	R	1097	AI228729			ESTs
21567	R	707	AI101159			ESTs
21570	B	762	AI104683			ESTs
21574	N	146	AA852038			ESTs
21575	E	1499	X55298	Biosynthesis and degradation of glycoprotein	HHs:ribophorin II	Rat ribophorin II mRNA
21586	G,I	1521	X97772			R.norvegicus mRNA for D-3-phosphoglycerate dehydrogenase
21657	B	1507	X61381			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21660	M	863	AI169751			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21661	M	968	AI176479			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21663	B	1635	NM_017126		ferredoxin 1	ferredoxin 1
21672	C	222	AA891789			ESTs
21682	P,Q	1609	NM_013154		CCAAT/enhancerbinding, protein (C/EBP) delta	CCAAT/enhancerbinding, protein (C/EBP) delta
21683	P	1609	NM_013154		CCAAT/enhancerbinding, protein (C/EBP) delta	CCAAT/enhancerbinding, protein (C/EBP) delta

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21695	A,I	240	AA892506			ESTs, Weakly similar to coronin-like protein [R.norvegicus]
21696	C	1724	NM_024152			Rattus norvegicus ADP-ribosylation factor 6 mRNA, complete cds
21707	A,C,E,N	176	AA859722			ESTs
21709	Q	1334	D29683		Hsp:ENDOTHELIN-CONVERTING ENZYME 1	Rat mRNA for endothelin-converting enzyme, complete cds
21717	E	131	AA850480			ESTs
21740	B,M,Q	986	AI176810			ESTs
21798	K	329	AA926365			ESTs, Moderately similar to AF151827_1 CGI-69 protein [H.sapiens]
21799	E	730	AI102576			ESTs
21818	I	491	AF036537			Rattus norvegicus homocysteine respondent protein HCYP2 mRNA, complete cds
21823	E	1119	AI229906			ESTs
21893	E	1302	AI237713			ESTs, Moderately similar to Y101_HUMAN HYPOTHETICAL PROTEIN KIAA0101 [H.sapiens]
21909	H	210	AA891161			ESTs
21950	G	570	AI013861			Rattus norvegicus 3-hydroxyiso-butyrate mRNA, 3' end
21976	R	379	AA946011			ESTs
21977	A,G	1432	S46785			Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21978	A,M	298	AA924289			Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds
21980	H	264	AA893454			ESTs
22038	A,C,D	1297	AI237609			ESTs
22042	P	390	AA946476			ESTs
22046	S	331	AA942726			ESTs
22051	E	275	AA899498			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
22077	A	1003	AI177099			ESTs, Highly similar to serine protease [H.sapiens]
22099	A	727	AI102258			ESTs, Moderately similar to BI54_MOUSE BRAIN PROTEIN I54 [M.musculus]
22124	J	223	AA891790			ESTs
22135	R	887	AI170821			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
22151	B,E,Q	521	AI009115			ESTs
22177	J	753	AI103730			ESTs
22197	A,C	1031	AI178527			ESTs
22204	K	886	AI170820			ESTs
22212	A	1268	AI236294			ESTs, Highly similar to translation initiation factor eIF6 [M.musculus]
22224	S	323	AA925869			ESTs
22235	L	294	AA924152			ESTs, Moderately similar to AF135422_1 GDP-mannose pyrophosphorylase A [H.sapiens]
22266	E,K	373	AA945601			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22321	B,I,M,Q	1372	J02962			Rat IgE binding protein mRNA, complete cds
22338	A	345	AA943896			ESTs
22368	A,Q	348	AA944157			ESTs
22370	S	349	AA944158			ESTs
22375	R	1121	AI230046			ESTs
22379	L	1156	AI231448	Glycolysis / Gluconeogenesis,Pentose phosphate cycle,Starch and sucrose metabolism	Glucose phosphate isomerase	ESTs, Highly similar to G6PI_MOUSE GLUCOSE-6-PHOSPHATE ISOMERASE [M.musculus]
22392	S	351	AA944269			ESTs, Weakly similar to es 64 [M.musculus]
22395	A	352	AA944289			ESTs
22397	F	353	AA944304			ESTs
22412	E	1702	NM_022392			Rattus norvegicus growth response protein (CL-6) mRNA, complete cds
22416	S	354	AA944380			ESTs
22432	A,C	895	AI171263			ESTs, Highly similar to FBRL_MOUSE FIBRILLARIN [M.musculus]
22443	J	1284	AI236761			ESTs
22457	A	358	AA944572			ESTs, Weakly similar to T2D7_RAT TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT [R.norvegicus]
22487	A,F,H	731	AI102578			ESTs, Highly similar to I49523 Mouse primary response gene B94 mRNA, 3'end - mouse [M.musculus]
22503	L	359	AA944823			ESTs
22512	M,P	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22513	F,M	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22514	M,P	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22515	M	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22516	M,P	796	AI113046		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22531	E	361	AA944943			ESTs
22534	E	310	AA925045			ESTs
22540	R	304	AA924630	Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism	HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA_RAT D-3 PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]
22548	L	364	AA945031			ESTs
22554	A,E,G,O	366	AA945076			ESTs
22558	A,E	368	AA945123		Hydroxyacid oxidase 1 (glycolate oxidase)	EST
22559	A,D	839	AI169007			ESTs
22566	E	1007	AI177122			ESTs
22569	A	1073	AI179979			ESTs
22570	R	369	AA945238			ESTs
22582	A,G	1605	NM_013120		Glucokinase regulatory protein	Glucokinase regulatory protein
22598	M	811	AI137506			ESTs, Weakly similar to SPI-2 serine protease inhibitor [R.norvegicus]
22603	E	494	AF044574			Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds
22619	B,E,Q	531	AI009825			ESTs
22620	S	316	AA925258			ESTs
22625	J	374	AA945704			ESTs
22679	A	332	AA942731			ESTs
22681	J	357	AA944413			ESTs
22683	A	970	AI176484			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22695	H	1032	AI178531			ESTs
22713	K	378	AA945904			ESTs
22717	L	1257	AI235948			ESTs, Highly similar to entactin [R.norvegicus]
22722	O	804	AI137211			ESTs
22725	Q	283	AA900506			ESTs, Highly similar to TS24_MOUSE PROTEIN TSG24 [M.musculus]
22737	S	465	AA998660			ESTs
22770	A	387	AA946428			ESTs
22806	E,Q	551	AI012174			ESTs, Moderately similar to hypothetical protein [H.sapiens]
22835	L	1079	AI180367			Rattus norvegicus small zinc finger-like protein (TIM10) mRNA, complete cds
22840	N	528	AI009676			ESTs
22862	H	227	AA891944			ESTs
22876	C	917	AI172041			ESTs, Moderately similar to CGI-137 protein [H.sapiens]
22877	A,C,D	1045	AI178819			ESTs, Moderately similar to CGI-137 protein [H.sapiens]
22897	P	290	AA901107			ESTs
22898	L,P	290	AA901107			ESTs
22906	L,N	944	AI175790			ESTs
22918	B,Q	29	AA800243			ESTs, Moderately similar to cell death activator CIDE-A [M.musculus]
22928	A,F	328	AA926262			ESTs
22929	A,L	670	AI071578			ESTs
22930	A	670	AI071578			ESTs
22931	A	777	AI105417			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22957	R	764	AI104897		HMm:mitogen activated protein kinase kinase 3	ESTs, Moderately similar to meningioma expressed antigen 11 [H.sapiens]
22961	E	1064	AI179519			ESTs
22966	B	1128	AI230320			ESTs
23000	H	178	AA859933			ESTs
23005	F,P	334	AA942770			ESTs
23013	I	1137	AI230743			ESTs, Weakly similar to ACTC_HUMAN ACTIN, ALPHA CARDIAC [R.norvegicus]
23030	L	305	AA924763			ESTs
23032	K	976	AI176596			ESTs
23033	G	179	AA859938			ESTs
23043	N	1051	AI178968			ESTs, Weakly similar to URB1_RAT DNA BINDING PROTEIN URE-B1 [R.norvegicus]
23044	A,H	490	AF034218			Rattus norvegicus hyaluronidase (Hyal2) mRNA, complete cds
23047	H	230	AA892027			ESTs
23075	A	844	AI169166			ESTs
23077	H	1015	AI177489			ESTs
23082	A	980	AI176648			ESTs
23099	C	789	AI112365			ESTs, Highly similar to mm-Mago [M.musculus]
23106	Q,R	825	AI145081		Mini chromosome maintenance deficient 4 homolog (S. cerevisiae)	ESTs, Highly similar to cell division control protein CDC21 [H.sapiens]
23120	C,D	1070	AI179857			ESTs, Weakly similar to UB5D_RAT UBIQUITIN-CONJUGATING ENZYME E2-17 KD 4 [R.norvegicus]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23125	B,Q	1172	AI232266			ESTs
23128	E	561	AI013011			ESTs
23139	H	1076	AI180040			ESTs
23160	C,L	960	AI176319		HMm:nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Rattus norvegicus I-kappa-B-beta mRNA, complete cds
23170	E	850	AI169317			ESTs, Weakly similar to C43H8.1 [C.elegans]
23173	I	312	AA925057			ESTs, Highly similar to CRIP_MOUSE CYSTEINE-RICH INTESTINAL PROTEIN [R.norvegicus]
23182	F,N	1141	AI230981			ESTs
23183	O	819	AI144586			Rattus norvegicus evectin-1 (EVT1) mRNA, complete cds
23184	C	974	AI176554			ESTs
23220	O	1319	AJ000347	Sulfur metabolism	HMm:bisphosphate 3'-nucleotidase 1	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase
23229	C	1229	AI234038			ESTs
23230	A,H,N	1266	AI236146			ESTs
23243	E	138	AA851803			ESTs
23245	Q	1066	AI179570			ESTs
23260	C,D	856	AI169617			ESTs, Highly similar to Bop1 [M.musculus]
23261	A,C,D	314	AA925145			ESTs
23299	C	989	AI176839			ESTs
23302	I,N	1516	X78949	Arginine and proline metabolism	HMm:procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	R.norvegicus mRNA for prolyl 4-hydroxylase alpha subunit

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23304	E	1153	AI231310	Arginine and proline metabolism	HMm:procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	R.norvegicus mRNA for prolyl 4-hydroxylase alpha subunit
23315	E,R	239	AA892425			ESTs
23321	A	247	AA892821			Rattus norvegicus aiar mRNA for androgen-inducible aldehyde reductase, complete cds
23322	A	247	AA892821			Rattus norvegicus aiar mRNA for androgen-inducible aldehyde reductase, complete cds
23324	E	181	AA859980			ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
23325	A	928	AI172405			ESTs
23331	J	1210	AI233457			ESTs, Highly similar to Mlark [M.musculus]
23337	E,O	520	AI009096			Rattus norvegicus double-stranded RNA binding protein p74 mRNA, complete cds
23362	O	1616	NM_013216		Ras homolog enriched in brain	Ras homolog enriched in brain
23380	A	141	AA851961			ESTs
23390	D,G	927	AI172328			ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
23435	C	1112	AI229502			ESTs, Highly similar to KIAA0601 protein [H.sapiens]
23437	A,O	661	AI071166			ESTs
23438	C,J	745	AI103101			ESTs, Highly similar to F25965 1 [H.sapiens]

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23445	A,D,F	1571	NM_012792		Flavin-containing monooxygenase 1	Flavin-containing monooxygenase 1
23448	B	315	AA925167			ESTs
23449	B,Q	987	AI176828			ESTs
23491	H,N,O	1681	NM_019359		acidic calponin	acidic calponin
23494	N	888	AI170967			ESTs
23499	A	393	AA955249			EST
23500	A,S	183	AA860010			ESTs
23511	A	1697	NM_022294			ESTs
23515	L	1063	AI179498			ESTs, Highly similar to S23B_HUMAN PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM B [H.sapiens]
23522	A,F	1552	NM_012615	Arginine and proline metabolism,Urea cycle and metabolism of amino groups	Ornitine decarboxylase	Ornitine decarboxylase
23523	A	1552	NM_012615	Arginine and proline metabolism,Urea cycle and metabolism of amino groups	Ornitine decarboxylase	Ornitine decarboxylase
23555	M,P	394	AA955443			ESTs
23558	A	400	AA956170			ESTs, Weakly similar to NDKA_RAT NUCLEOSIDE DIPHOSPHATE KINASE A [R.norvegicus]
23567	J	1042	AI178746			ESTs
23584	A,B	392	AA955071			ESTs
23587	J	977	AI176598			ESTs

TABLE 1						Document Number 1650775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23606	H,N	1714	NM_022867			Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23608	E	1201	AI233190			Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23612	A	880	AI170751			ESTs
23626	N	395	AA955540			ESTs
23627	S	628	AI045624			ESTs, Moderately similar to AF151890_1 CGI-132 protein [H.sapiens]
23633	A	706	AI101130			ESTs
23651	I	1582	NM_012881		Sialoprotein (osteopontin)	Sialoprotein (osteopontin)
23656	R	616	AI044533			ESTs
23678	C	1674	NM_019290		B-cell translocation gene 3	B-cell translocation gene 3
23679	A,C,D,F	1674	NM_019290		B-cell translocation gene 3	B-cell translocation gene 3
23698	E	1532	NM_012489		Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal
23709	H,K	1603	NM_013113		ATPase Na+/K+ transporting beta 1 polypeptide	ATPase Na+/K+ transporting beta 1 polypeptide
23710	H	1135	AI230614		ATPase Na+/K+ transporting beta 1 polypeptide	ATPase Na+/K+ transporting beta 1 polypeptide
23711	H	1603	NM_013113		ATPase Na+/K+ transporting beta 1 polypeptide	ATPase Na+/K+ transporting beta 1 polypeptide
23762	R	404	AA956431			ESTs, Highly similar to Lsm5 protein [H.sapiens]
23767	A	1295	AI237207			ESTs
23843	E,R	412	AA957410			ESTs
23847	B	405	AA956723			EST

TABLE 1						Document Number 1650775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23854	G,I	1514	X78327			R.norvegicus (Sprague Dawley) ribosomal protein L13 mRNA
23855	B,C	1287	AI236773			ESTs
23868	F	1543	NM_012551		Early growth response 1	Early growth response 1
23869	F	1543	NM_012551		Early growth response 1	Early growth response 1
23872	F	1543	NM_012551		Early growth response 1	Early growth response 1
23884	A	1422	M73714	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Phenylalanine metabolism, Propanoate metabolism, Pyruvate metabolism	aldehyde dehydrogenase 4, liver microsomal (class 3)	Rat microsomal aldehyde dehydrogenase mRNA, complete cds
23885	E	866	AI170007			ESTs
23888	I	241	AA892520			ESTs
23889	M	241	AA892520			ESTs
23890	B	406	AA956864			ESTs
23945	F	409	AA957071			ESTs, Highly similar to Bcl-2-interacting protein beclin [H.sapiens]
23955	A	1103	AI229178			ESTs
23961	A,D	1640	NM_017181	Tyrosine metabolism	fumarylacetoacetate hydrolase	fumarylacetoacetate hydrolase
23987	O	1496	X51615			ESTs
23989	B,Q	1072	AI179953			ESTs
24012	M,O	411	AA957335			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24024	Q	496	AF052695			Rattus norvegicus p55CDC mRNA, complete cds
24049	G	1010	AI177341			ESTs, Highly similar to CGI-10 protein [H.sapiens]
24051	L	414	AA957452			EST
24079	H	935	AI175423			ESTs
24112	O	514	AI008773			ESTs
24126	R	415	AA957708			ESTs
24146	E	859	AI169668			ESTs, Weakly similar to hypothetical protein [H.sapiens]
24161	E	150	AA858588			ESTs
24162	A	847	AI169279			ESTs
24200	N	555	AI012356			ESTs
24219	A	1395	L27843		protein tyrosine phosphatase 4a1	Rattus norvegicus tyrosine phosphatase (PRL-1) mRNA, complete cds
24227	L	871	AI170385			ESTs
24228	M	30	AA800318			ESTs, Weakly similar to A1AT_RAT ALPHA-1-ANTIPROTEINASE PRECURSOR [R.norvegicus]
24234	J	1469	U63923			Rattus norvegicus NADPH-dependent thioredoxin reductase (TRR1) mRNA, complete cds
24235	A,D,J	213	AA891286			Rattus norvegicus NADPH-dependent thioredoxin reductase (TRR1) mRNA, complete cds
24236	C,L	967	AI176473			ESTs
24237	F,M	44	AA817726			ESTs

TABLE 1						Document Number 1650775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24246	G	419	AA963703			ESTs, Highly similar to cell cycle protein p38-2G4 homolog [H.sapiens]
24264	A	1593	NM_012999		Subtilisin - like endoprotease	Subtilisin - like endoprotease
24268	E	924	AI172281			ESTs
24284	A	1715	NM_022869			Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp140 mRNA, complete cds
24289	B,Q	399	AA955986	Galactose metabolism	Galactokinase	ESTs, Highly similar to galactokinase [M.musculus]
24296	E	1360	H32867			ESTs, Highly similar to steroidogenic acute regulatory protein [R.norvegicus]
24321	A,D,G	1178	AI232340			ESTs
24323	P	763	AI104798			ESTs, Moderately similar to GTM1_RAT GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus]
24367	R	401	AA956247			EST
24368	R	1080	AI180392			ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]
24369	R	346	AA944011			ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]
24375	A,D	766	AI104979			ESTs, Moderately similar to nucleolar protein p40 [H.sapiens]
24381	S	403	AA956301			ESTs
24388	C,D,I,R	1286	AI236772			ESTs
24434	A	1710	NM_022704			Rat mannose-binding protein C (liver) mRNA, complete cds
24442	O	1708	NM_022667			Rat matrin F/G mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24453	F	1560	NM_012690		P-glycoprotein 3/ multidrug resistance 2,P-glycoprotein/multidrug resistance 1	P-glycoprotein 3/ multidrug resistance 2
24458	A	1711	NM_022706			Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds
24501	D	1167	AI232006			Rattus norvegicus translation elongation factor 1-delta subunit mRNA, partial cds
24508	E	1416	M34643			Rat neurotrophin-3 (HDNF/NT-3) mRNA, complete cds
24577	A	1498	X55153			ESTs, Highly similar to RLA2_RAT 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus]
24589	E,P	1558	NM_012674		Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic
24597	C	1625	NM_017040		Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
24645	A	1484	V01225	Starch and sucrose metabolism	HMm:amylase 2, pancreatic	Rat pancreatic amylase mRNA, partial coding sequence
24651	P	1426	M83678			Sprague-Dawley (clone LRB10) RAB13 mRNA, 3'end
24654	E	100	AA819333			Sprague-Dawley (clone LRB2) RAB16 mRNA, complete cds
24670	G	1642	NM_017189		asialoglycoprotein receptor 2	asialoglycoprotein receptor 2
24707	E,O	1561	NM_012693	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450 IIA2	Cytochrome P450 IIA2
24710	C	1430	M98820	interact6-1	Interleukin 1 beta	Rat interleukin 1-beta mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24721	Q	99	AA819306			ESTs
24722	G	1564	NM_012725		Plasma kallikrein	Plasma kallikrein
24771	A,G	1626	NM_017047		Solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1
24779	F	1375	J03863	Cysteine metabolism, Glycine, serine and threonine metabolism, Oxidative phosphorylation	HHs:serine dehydratase	Rat serine dehydratase (SDH2) mRNA, complete cds
24810	F,G	1391	L22339	Sulfur metabolism	sulfotransferase, phenol preferring 2	Rat N-hydroxy-2-acetylaminofluorene (ST1C1) mRNA, complete cds
24811	G	1391	L22339	Sulfur metabolism	sulfotransferase, phenol preferring 2	Rat N-hydroxy-2-acetylaminofluorene (ST1C1) mRNA, complete cds
24826	P	1421	M63991			Rat thyroxine-binding globulin (TBG) mRNA, 3' end
24860	K,S	1403	M13506	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	Hsp:UDP-GLUCURONOSYLTRANSFERASE 2B1 PRECURSOR, MICROSOMAL	Rat liver UDP-glucuronosyltransferase, phenobarbital-inducible form mRNA, complete cds
24883	A	1677	NM_019293	Nitrogen metabolism	carbonic anhydrase 5	carbonic anhydrase 5
25024	F	1353	E03229			
25052	A,F,M,P	1390	L22190			
25054	A	1396	L36460			
25055	K	1398	M11251			
25056	K,L	1402	M13234			
25069	F,G	1440	S82820			
25077	Q	1453	U20643			

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
25083	P	1473	U72632	Arginine and proline metabolism,Glycine, serine and threonine metabolism,Histidine metabolism,Phenylalanine metabolism,Tryptophan metabolism,Tyrosine metabolism,beta-Alanine metabolism	Hsp:MEMBRANE COPPER AMINE OXIDASE	
25098	J	1	AA108277			
25183	K	495	AF050159		insulin receptor substrate 2	
25198	J	1689	NM_021754			
25203	E	501	AF079873			
25246	M	1321	AJ011607			
25257	C,I	1328	D13623			
25290	M,O	1339	D42148			
25313	I	1347	D87991			
25370	B,Q	1387	L16995			
25379	Q	1394	L26292			
25397	E	1401	M12822			
25409	E	1408	M18527			
25410	E	1409	M18528			
25411	E	1410	M18529			
25413	E	1411	M18531			
25480	A,G	1432	S46785			
25525	P	1437	S72505	Glutathione metabolism	Hsp:GLUTATHIONE S-TRANSFERASE YC-1	
25567	A,J	1441	S85184			
25615	E	1466	U58466			

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
25618	M	1470	U64705			
25619	M	1470	U64705			
25632	G	1476	U75405			
25644	E	1479	U77931			
25675	A	1493	X14181			
25702	A	1502	X58465			
25705	H	1504	X59375			
25706	L	1506	X59608			
25718	I,O	1508	X62145		ribosomal protein L8	
25725	K	1510	X62660			
25747	A,F	1518	X81448			
25768	Q	1520	X94769			
25777	E	1523	Y08355			
25802	E,I	1352	E02315			
25814	H	1696	NM_022268			
25852	L	1305	AI638998			
25892	G	1309	AI639101			
25907	J	1313	AI639167			
25938	B	1314	AI639281			
26088	E	291	AA901152			
26109	S	441	AA997009			
26123	D	511	AI008396			
26133	M	532	AI009950			
26147	E	563	AI013387			
26152	N	576	AI028938			
26190	E,R	688	AI072578			
26280	Q	1082	AI227562			
26288	E	1134	AI230577			
26320	M	1242	AI234927			

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
26368	E	1367	H34047			
26369	C,D	1369	H34687			

TABLE 2	Document Number 1650775
Comparison	**Comparison Code**
General Toxicity: Amitryptiline, ANIT, APAP, CCl4, Diclofenac, Indomethacin, Valproate, Untreated Rats, Various Vehicles, WY-14643, Cyproterone Acetate, and Estradiol	A
Hepatitis-inducing and NSAIDS: Diclofenac and Indomethacin	B
Necrosis and Fatty Liver: Carbon Tetrachloride and Valproate	C
Necrosis With and Without Fatty Liver: Carbon Tetrachloride, Valproate, and Acetaminophen	D
Protein Adduct Formers: Valproate and Diclofenac	E
ANIT	F
Late Acetaminophen	G
Early Acetaminophen	H
Late Carbon Tetrachloride	I
Early Carbon Tetrachloride	J
Late Cyproterone Acetate	K
Early Cyproterone Acetate	L
Late Diclofenac	M
Early Diclofenac	N
Estradiol	O
Late Indomethacin	P
Early Indomethacin	Q
Valproate	R
WY-14643	S

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21471	30.43	93.54	75	-42.67	24.83
13203	35.33	61.64	74	-31.14	29.79
19909	22.08	33.51	73	-15.41	29.38
4553	13.83	18.08	72	1.43	6.49
15301	124.27	140.5	77	5.51	36.16
20456	42.5	31.85	70	7.46	20.45
23679	57.12	66.55	72	8.07	7.49
14693	37.57	38.27	72	9.49	11.63
12471	26.73	25.33	73	9.55	21.73
923	60.74	80.74	71	9.6	6.57
15647	49.51	40.73	72	10.9	23.58
6322	45.84	55.48	70	12.42	10.76
16314	48.7	48.51	70	12.45	16.75
25052	90.08	154.89	70	14.05	18.5
2164	57.65	53.74	73	14.96	17.31
16006	58.93	36.27	80	15.18	19.39
25054	45.65	42.59	72	15.37	40.01
6410	4.65	23.5	70	15.8	61.49
23500	39.03	35.28	70	16.65	11.6
16312	39.06	24.35	75	17.24	10.59
19843	2.55	18.74	74	17.7	10.31
14996	58.1	47.71	71	20.43	22.52
16085	60.79	45.9	70	21.59	14.6
17982	49.3	27.48	70	23.22	18.41
6226	46.81	36.97	71	23.54	10.28
9326	6.05	16.52	70	24.18	25.4
15055	-7.1	34.32	70	24.3	26.9
351	94.58	92.7	71	26.37	19.43
1126	48.74	21.68	72	26.96	14.06
20161	87.17	88.37	76	27.44	26.92
8766	-14.3	48.76	75	27.97	35.81
23511	12.84	20.12	72	29.05	16
5461	77.51	74.15	71	29.28	16.66
12216	-22.58	61.28	71	29.83	80.65
5384	100.6	91.07	76	30.03	29.52
18389	43.98	46.66	74	31.53	26.82
21695	45.44	55.44	72	31.53	16.62
11357	17.28	18.76	73	31.76	16.7
14424	567.82	812.48	70	32.4	34.02
9331	60.44	27.33	70	33.81	15.06
23767	23.85	17.49	71	34.2	50.3
15862	62.08	31.33	71	34.72	12.31
20449	117.61	143.09	71	35.82	9.2
10248	68.54	26.33	77	36.88	16.24

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23082	23.23	17.75	71	37.04	12.65
9425	17.36	27.44	71	37.87	17.12
16730	73.58	39.38	73	39.09	20.24
9583	161.94	162.1	73	39.37	25.85
11563	71.92	56.8	70	39.98	27.02
352	130.52	119.67	76	40.04	18.99
6604	24.19	16.7	74	41.3	15.53
7243	91.67	50.42	74	41.4	14.59
17709	71.49	47.04	70	41.77	28.89
1583	62.93	26.33	71	41.81	9.01
761	28.63	19.45	70	43.38	21.32
3849	81.84	39.76	71	43.61	16.59
24284	65.8	20.86	74	45.29	13.2
3207	25.59	109.41	70	45.31	54.06
21707	108.81	66.66	72	45.32	39.4
17589	85.64	50.71	71	46.93	27.53
22212	112.59	77.44	70	47.96	21.25
5175	72.78	115.19	71	48.48	31.56
7299	220.49	225.32	77	49.33	34.75
19678	3.58	46.62	75	49.59	34.93
21088	58.85	18.82	72	51.63	11.12
15892	152	118.78	75	52.52	42.58
14353	84.25	29.24	74	53.47	12.39
11527	119.25	79.46	70	54.98	27.79
13749	38.3	29.23	73	55.43	20.89
4281	38.95	21.16	70	57.15	17.8
353	194.24	177.12	76	57.46	26.37
14206	41.14	16.67	73	57.71	14.34
16080	207.65	183.99	77	58.82	28.68
6682	53.78	37.44	70	59.02	19.46
825	42.12	20.91	71	59.35	17.09
7918	90.4	45.57	71	60.65	23.06
21150	138.34	101.42	71	64.19	46.67
7531	57.13	26.96	70	64.99	18.47
22487	81.97	69.8	71	66.94	27.76
24264	112.04	51.05	72	67.41	29.12
22077	46.19	26.57	70	67.77	24.16
21209	174.43	157.48	73	70.46	46.49
20772	102.74	37.31	72	70.49	15.59
8600	33.46	36.07	72	71.84	38.68
9826	49.36	28.75	70	72	22.77
17688	108.65	39.15	70	72.62	19.69
6640	40.46	39.18	74	73.64	29.52
3074	75.98	91.66	70	73.84	44.71

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
4473	54.98	25.48	70	74.37	21.06
354	227.5	203.23	77	74.89	23.89
23522	107.75	42.24	73	74.91	18.29
15299	176.87	143.39	75	75.35	20.66
13166	145.19	92.31	71	75.39	33.67
7936	59.06	21.73	70	76.33	18.71
17819	57.46	25.12	71	76.84	20.15
17908	191.58	159.91	71	77.06	30.42
7681	125.85	57.35	71	77.88	39.68
23633	66.31	40.72	70	78.12	28.98
19508	49.65	31.49	70	78.53	32.19
9541	166.47	123.33	72	79.59	34.68
16446	58.49	21.61	71	80.2	20.86
17377	119.83	80.06	72	82.65	37.63
20801	136.04	60.94	71	83	38.58
7352	164.48	94.53	70	83.91	38.34
2901	63.21	31.06	71	84.9	24.78
15156	85.12	43.67	71	85.31	23.45
22877	140.94	62.91	71	85.66	25.88
15207	112.17	89.27	73	85.8	32.15
9627	65.98	37.05	73	86.7	25.5
4017	71.08	40.29	70	86.72	27.99
4944	252.32	217.46	76	86.84	38.34
3073	78.22	126.03	72	87.19	58.64
5046	99.33	75.05	70	91.34	37.3
3713	66.05	38.37	71	91.52	27.81
11576	56.54	27.2	75	92.19	28.07
1246	57.52	28.55	70	92.34	25.09
15382	699.61	884.63	73	92.89	30.78
18109	105.09	108.04	71	93.58	44.98
18906	66.76	34.6	72	93.87	22.06
16324	65.53	39.09	72	94.25	27.97
7903	31.76	35.55	72	94.94	65.97
7063	179.3	93.83	74	95.16	22.48
9053	60.23	42.49	72	97.12	25.77
5813	67.41	28.11	70	97.48	35.73
9245	39.62	45.11	73	97.55	55.74
16081	293.48	225.5	78	97.81	34.89
19085	146.97	54.5	71	98.39	27.86
3189	48.18	30.77	70	99.15	55.31
12655	74.53	78.23	70	99.85	45.15
5219	54.76	44.93	70	100.79	47.29
7062	157.19	68.98	70	101.14	24.11
6820	132.9	40.9	71	101.15	18.57

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21025	52.78	49.73	75	102	38.88
14746	72.12	42.89	70	102.6	35.3
11745	127.84	29.61	71	102.7	19.78
20035	330.62	323.46	73	105.65	47.24
12587	72.78	43.64	72	105.95	35.48
2372	89.09	42.56	70	107.07	30.91
2383	87.59	39.36	72	108.56	32.43
2532	28.55	57.57	72	109.2	73.94
11959	91.5	26.27	70	109.84	20.36
24375	200.33	108.66	72	110.42	32.85
15884	135.81	86.11	70	111.91	36.88
2576	81.51	44.81	71	112.47	36.08
23955	98.48	60.26	72	113.59	36.89
5008	152.54	61.16	71	113.65	24.98
20891	174.25	85.84	72	114.45	35.06
18390	78.44	44.36	70	116.93	42.8
1844	172.33	73.68	70	117.06	23.94
17591	177.66	76.44	70	119.35	26.88
22038	178.88	77.12	70	119.93	32.92
20874	102.83	26.99	76	120.76	19.57
17844	225.91	107.09	73	120.8	50.32
11691	80.29	49.49	73	124.21	42.81
19086	192.42	71.46	72	124.7	32.65
14937	93.31	50.67	75	125.88	34.64
20513	76.12	59.17	72	127.29	74
6037	90.3	39.56	73	127.31	44.99
12332	24.75	72.13	73	128.95	100.98
17335	99.84	36.82	73	129.97	30.57
134	71.14	58.38	77	133.41	39.47
7784	109.76	36.32	70	134.08	25.84
25567	222.63	133.25	70	134.17	40.36
4951	296.48	152.65	74	135.21	102.87
13351	87.72	56.78	76	135.45	45.49
22432	207.69	93.56	71	137.45	35.3
3075	134.78	146.57	74	138.67	65.46
16134	88.41	44.61	74	139.59	36.27
18660	99.04	62.72	74	141.07	60.13
17225	208.62	72.16	71	141.32	36.37
10509	91.25	50	70	142.42	48.95
6190	108.44	39.25	71	142.68	30.93
17393	216.6	101.01	70	144.48	27.96
22197	295.18	157.65	75	144.6	54.77
19952	98.31	43.39	75	145.63	36.13
1690	206.44	90.45	70	147.21	36.46

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23044	188.12	53.18	74	148	23.7
22931	50.06	64.25	72	148.05	101.64
14776	103.46	45.74	74	148.29	40.54
14051	218.89	97.53	70	149.85	36.11
22569	103.93	53.65	76	150.14	42.57
11403	485.69	353.08	74	150.23	94.34
13762	105.01	72.99	71	151.26	47.6
14074	72.32	60.1	74	153.35	74.91
18960	120.13	59.4	71	156.6	44.43
20889	193.77	86.18	70	156.83	37.64
4084	127.09	64.08	71	158.37	49.57
18854	124.79	56.31	70	158.52	38.36
20735	294.63	147.51	80	164.19	33.2
14181	117.28	41.72	73	165.97	41.05
24883	122.66	51.37	75	165.99	38.66
15933	192.2	65.93	70	166.13	35.32
18792	112.37	55.57	73	167.2	48.33
10544	240.01	60.23	77	167.22	32.41
14208	98.76	46.96	77	167.76	48.04
20734	292.65	126.84	78	169.42	39.52
17334	283.45	131.16	76	170.46	50.64
22457	319.78	159.2	71	170.89	83.07
21978	127.23	34.44	75	172	37.41
20088	138.87	33.78	75	173.08	29.79
15300	301.38	143.25	73	174	53.02
16364	109.25	72.42	74	174.33	56.68
8829	280.85	107.19	74	174.35	39.95
1007	71.78	95.85	73	174.52	94.52
6443	130.76	76.39	77	174.54	46.87
17154	237.49	69.3	73	174.79	36.28
6473	107.85	42.8	72	175.56	60.84
2335	121.97	52.51	71	175.91	56.34
12450	90.03	92.4	75	181.36	63.89
16700	116.46	131.83	75	181.51	86.73
15955	105.87	86.17	73	183.02	74.51
23523	254.3	77.51	75	184.72	39.26
15900	300.11	139.69	72	184.95	58.44
10545	272.15	72.91	74	188.26	35.42
16982	503.02	283.02	72	188.67	203.36
12848	147.36	47.97	70	188.99	42.1
5749	219.23	62.17	70	189.76	42.51
15004	289.65	146.93	71	189.87	51.07
23075	307.83	118.82	72	190.09	58.23
23584	123.89	91.92	73	190.24	73.31

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
14997	311.34	155.46	77	193.29	31.96
7617	133.32	123.53	70	193.38	108.54
11404	425.93	237.07	74	193.8	75.57
14095	145.71	64.97	77	194.48	44.06
16766	128.68	62.34	72	197.3	64.57
13757	132.12	63.33	72	197.76	47.88
3981	165.72	126.27	71	199.27	79.29
6632	374.92	164.24	76	199.58	56.28
22770	344.97	196.08	74	199.66	52.17
1099	159.6	51.35	71	200.56	47.88
15170	132.07	62.08	79	201.16	44.18
21125	104.89	85.5	74	205.52	74.23
23499	149	73.65	71	206.76	68.16
16765	131.63	64.51	74	208.95	60.5
23321	173.83	57.63	71	209.49	31.61
18908	94.04	112.32	72	209.75	126.49
4360	159.27	76.32	72	212.18	102.53
5027	165.48	78.52	73	212.59	52.82
14007	147.14	73.93	77	213.84	62.97
4719	153.89	88.13	74	216.28	70.99
9754	78.35	97.33	75	218.88	111.68
5867	342.61	167.79	70	219.32	57.15
16859	374.28	189.12	73	220.43	60.14
24434	132.32	69.32	71	226.73	56.25
22683	206.07	65.39	71	228.15	41.78
13963	218.82	179.67	72	228.18	75.69
11179	165.79	72.22	70	230.16	61.5
23445	110.29	87.9	82	231.61	62.42
18115	174.03	108.43	71	231.75	102.05
11429	189.45	42.84	72	232.42	40.03
11520	175.16	127.89	72	233.8	92.23
7927	202.04	106.05	70	234.79	57.37
22099	137.03	97.01	71	235.76	97.02
7888	376.09	171.23	72	236.43	56.75
17496	75.49	73.53	76	239.51	173.47
11742	161.82	79.25	71	239.68	82.64
6855	194.24	59.54	71	245.57	58.27
22928	87.17	110.53	70	245.88	162.18
7064	397.22	140.47	77	247.28	40.15
10879	202.31	103.86	70	248.56	66.82
20757	401.81	200.88	71	249.74	57.1
7113	200.31	111.11	74	250.23	78.75
11635	186.84	60.17	75	254.75	47.63
135	174.94	73.25	78	256.19	65.78

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
24235	390.14	159.67	70	259.52	50.47
1479	205.28	61.98	72	261.61	51.03
5923	172.52	80.09	78	262.06	70.65
15642	368.73	123.22	77	262.87	41.31
9336	140.36	75.51	72	264.38	147.6
23325	326.83	125.56	70	265.55	63.28
9063	214.94	71.54	74	266.92	47.88
23612	382.82	255.62	72	267.25	92.93
912	326.5	67.38	73	268	33.47
14506	208.78	65.03	70	272.49	69.62
5748	328.41	66.67	70	274.63	44.97
8477	399.36	174.12	71	275.64	90.8
11021	177.75	93.53	73	275.95	97.97
8630	206.38	87.63	72	276.18	71.7
12331	142.97	91.35	73	276.42	113.01
12694	196.38	106.12	70	280.6	91.59
23380	201.35	91.04	71	280.63	98.56
25747	406.23	174.62	79	281.96	48.12
3418	416.76	178.28	75	282.48	51.77
19298	475.37	243.42	71	283.29	78.74
23558	187.58	94.53	72	284.57	75.57
6366	365.38	251.12	70	289.81	76.83
14103	153.89	84.24	76	291.22	113.41
24219	410.88	138.62	75	297.66	69
1929	232.96	81.98	71	298.56	77.17
5863	225.48	130.42	75	299.73	84.35
3504	395.85	157.69	70	301.1	58.36
4868	220.65	100.78	75	301.7	70.8
1753	235.94	62.13	72	304.05	74.62
22679	185.35	110.73	72	304.26	119.66
23230	431.68	274.8	77	305.51	73.66
17401	211.41	101.33	70	308.15	101.7
4179	444.58	228.79	73	308.58	63.03
24645	228.44	65.97	73	308.66	90.32
19679	212.7	94.25	74	309.08	79.13
8387	209.62	77.78	74	309.81	64.43
17324	236.31	65.13	73	311.13	52.23
1501	434.85	171.45	79	314.29	63.39
22582	224.5	87.58	71	316.36	75.3
25702	423.41	113.7	72	320.39	51.32
9399	222.67	63.69	76	320.67	86.48
3131	228.57	86.2	72	321.25	92.07
812	231.65	67.37	76	321.96	51.58
15519	303.98	284.36	71	322.04	142.67

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
1409	258.93	68.93	72	323.5	60.85
17049	207.81	93.01	77	324.1	63.71
7003	213.89	133.94	75	328.74	101.01
15612	208.41	106.4	71	329.06	202.57
851	259.03	53.32	76	331.68	47.82
4291	203.94	139.04	77	334.29	127.4
1478	262.27	68.1	74	334.41	51.89
7868	201.78	131.72	80	338.05	94.52
19469	284.04	59.16	72	342.98	50.36
15700	259.03	65.96	77	345.34	50.31
15197	263	83.78	70	348.89	85.31
2484	152.64	144.08	75	349.45	189.22
21396	274.52	76.97	73	354.24	57.86
15032	262.98	104.76	72	354.96	94.2
6825	321.55	146.79	71	355.67	98.41
14767	212.27	97.6	80	359.19	95.6
15136	482.9	133.86	71	361.06	68.44
2993	498.11	173.18	73	362.5	53.1
1175	211.25	155.83	72	367.03	107.25
16680	296.57	157.31	71	368.4	135.7
961	300.69	83.8	73	370.86	65.28
2696	463.19	111.26	71	371.94	59.78
17256	266.11	96.28	72	373.05	70.36
4937	305.59	112.68	74	375.59	89.26
18860	314.98	128.88	70	375.92	92.09
23884	312.54	72.12	70	379.68	59.35
17850	516.17	220.77	70	383.69	72.82
17175	504.94	132.64	72	384.43	64.15
12946	275.06	103.13	74	384.61	80.84
23322	308.64	91.46	73	385.69	58.02
16327	318.14	112.83	72	386.27	63.57
6824	820.68	540.91	70	386.87	102.09
1900	230.35	153.17	72	387.22	135.44
14869	290.26	114.01	70	388.39	93.33
15239	472.89	104.14	70	393.48	56.96
20694	256	155.8	75	396.34	127.36
6321	661.68	352.96	71	397.84	101.24
21157	628.44	255.63	70	401.01	132.71
1529	316.33	75.8	73	401.61	56.86
5934	166.87	133.41	76	401.67	162.84
18597	452.56	154.66	72	402.92	64.14
6801	284.93	123.62	70	403.58	114.82
8317	302.02	115.59	71	403.7	92.47
3959	651.41	284.48	73	404.94	125.39

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
6017	218.37	162.51	71	408.35	157.64
7785	309.16	154.16	71	411.11	92.69
18453	272.77	135.91	72	412.12	103.91
11157	347.22	111.72	73	412.71	76.32
2799	186.49	165.24	73	413.66	193.94
18606	551.54	140.45	71	415.6	65.98
25480	298.56	93.25	80	417.76	62.1
6554	327.78	86.42	75	418.15	72.16
22395	337.48	106	70	424.15	101.1
18861	353.52	146.94	71	431.18	96.34
556	363.95	72.87	72	431.39	47.74
15016	614.84	191.45	72	431.42	106
20707	297.52	182.87	72	432.6	110.59
6615	313.91	151.88	70	435.29	105.91
25675	559.03	149.18	71	435.84	78.46
24458	391.59	66.22	70	440.47	58.22
2264	348.28	114.55	70	442.01	101.65
811	339.77	83.76	80	442.46	54.75
14962	595.24	186.44	71	443.26	86.3
9905	351.99	86.2	73	443.66	62.13
4670	1011.12	757.17	70	449.34	279.51
15135	572.07	128.52	72	452.98	71.41
1877	381.72	99.89	72	455.58	70.01
2905	368.76	236.61	74	455.99	171.06
10176	362.61	131.62	73	458.21	78.68
8880	270.36	150.83	71	461.94	178.82
21977	333.82	102.68	78	464.63	71.57
19103	373.87	152.27	72	466.17	87.18
2505	361.86	109.11	73	466.31	72.15
7582	256.38	164.17	72	466.34	223.76
18001	369.81	89.98	72	467.77	75.36
15755	405.73	112.28	71	473.79	67.48
24577	583.7	137.54	73	474.11	65.9
20299	326.39	113.27	76	477.33	90.93
7697	273.75	100.92	83	481.09	117.81
18867	425.79	164.92	71	486.56	85.09
16726	386.57	78.35	71	489.29	90.61
18522	338.66	110.39	78	493.05	127.44
794	364.93	131.6	73	493.86	73.31
21097	596.6	213.78	72	494.87	76.63
11166	392.77	163.68	74	496.16	102.35
3823	819.94	253.21	84	496.62	131.46
20701	546.93	267.9	71	497.17	122.04
13283	374.45	137.36	71	498.65	90.97

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
14312	379.02	130.24	70	498.8	162.03
1561	489.56	192.41	70	503.1	74.48
11693	280.1	210.45	74	504.39	202.02
19470	355.43	120.62	75	507.23	102.75
20705	406.75	228.32	72	520.73	125.68
6060	377.46	110.54	75	524.04	95.02
4143	411.36	153.04	70	526.83	142.72
573	397.93	141.77	74	527.31	101.53
2111	431.14	135.97	70	535.18	95.74
6132	389.97	132.3	70	536.05	116.38
1531	432.89	99.85	74	537.37	84.23
13684	732.21	234.57	71	538.64	123.03
4914	320.44	176.4	77	542.57	159.28
16172	384.09	149.87	71	543.43	107
18661	375.83	155.78	71	546.25	136.03
14035	354.4	185.79	72	546.44	215.25
18452	376.32	156.49	75	548.91	124.57
10109	683.1	154.88	71	554.69	60.26
15113	422.52	185.06	72	557.21	136.1
12087	426.39	140.52	70	558.91	91.57
11492	398.17	152.29	73	559.08	143.79
14083	400.42	184.48	74	569.39	131.38
23961	487.24	102.51	71	571.23	72.66
6761	734.58	239.42	73	572.66	144.55
16993	402.56	131.25	80	574.27	86.25
11536	347.49	123.19	77	575.39	198.99
12312	415.93	131.04	75	579.26	98.18
20810	686.37	181.4	70	589.89	79.84
24771	441.44	127.76	75	592.18	94.5
6007	477.65	139.01	76	592.68	113.45
3145	432.3	212.79	72	610.87	178.16
12064	392.31	195.73	78	611.49	148.58
15080	468.83	133	74	613.82	131.38
22338	858.3	334.36	70	633.42	176.07
23437	417.21	173.85	75	633.59	238.89
20397	775.65	145.47	74	638.29	86.47
22930	206.34	282.8	72	638.83	389.14
5943	365.28	277.04	78	658.15	266.99
13088	440.35	191.07	72	659.11	130.73
3969	461.16	167.2	73	671.43	138.26
2536	229.18	164.07	75	680.76	402.5
8946	488.94	198.29	74	698.4	191.02
1173	454.86	255.52	73	701.71	147.85
6613	475.14	319.24	71	703.21	206.38

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
17847	587.34	146.42	73	728.57	116.89
19069	401.65	251.38	70	736.55	312.13
3121	582.17	314.22	75	743.82	177.43
2762	549.37	222.1	73	744.04	144.72
9191	353.85	236.51	80	747.6	226.01
17339	394.82	309.4	71	757.04	450.78
3365	465.6	196.26	75	759.09	201.02
5622	781.85	245.85	70	761.19	118.25
19729	390.13	332.32	78	764.27	355.89
9012	363.63	210.98	77	764.48	253.76
4193	592.69	173.22	72	771.85	108.77
8549	428.57	212.41	77	776.74	195.59
16190	633.77	300.61	71	788.33	198.05
6143	563.65	311.9	76	807.95	145.12
11228	611.37	254.64	71	817.25	249.82
19830	639.79	218.85	75	827.94	161.07
11504	659.77	278.75	70	831.93	222.74
2569	457.34	317.75	82	855.43	152.77
12160	812.82	573.26	70	864.88	230.19
21341	583.63	407.72	73	869.75	255.69
24321	471.3	256.45	83	871.6	204.88
14584	778.69	204.76	72	899.51	154.36
4440	592.51	190.31	81	903.2	141.99
17340	1192.58	780.31	70	918.51	258.08
2196	676.58	230.37	76	961.23	265.77
16879	875.19	424.83	74	998.63	195.4
14118	716.41	266.36	72	1006.89	263.75
20503	598.26	362.91	74	1021.64	320.28
12306	1122.58	844.77	71	1023.1	338.53
2911	675.36	278.69	72	1039.76	290.7
18796	825.55	557.51	70	1043.22	369.63
19732	639.42	377.16	74	1044.68	344.85
11205	763.23	299.36	72	1062.45	233.92
13634	1541.83	591.67	70	1065.68	230.26
8692	729.45	328.96	71	1075.69	284.09
22559	707.2	351.3	74	1078.43	298.05
9475	633.07	305.29	76	1091.11	321.49
6033	695.09	293.08	78	1093.71	230.15
7893	681.36	341.8	72	1123.77	299.15
3822	1790.91	546.55	78	1156.91	279.92
18910	691.91	316.7	77	1158.26	375.48
16703	811.27	347.36	78	1176.58	244.51
10984	769.03	347.66	74	1177.95	295.11
24162	935.19	218.55	71	1183.5	254.36

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
14960	1815.81	619.16	72	1189.85	282.97
22368	809.54	304.72	78	1204.44	255.44
14512	758.14	344.89	75	1207.73	316.98
22929	345.04	524.79	76	1263.79	749.31
6633	1158.38	523.64	70	1282.41	230.42
5899	868.41	419.97	75	1320.55	275.91
17027	885.56	416.43	74	1334.54	460.45
633	1120.93	302.27	71	1460.55	215.38
15240	1096.17	411.07	71	1507.99	426.62
3916	981.26	439.68	78	1583.55	340.89
22554	987.76	444.02	77	1595.12	393.47
3995	1025.02	387.98	75	1611.33	356.12
16885	1112.24	354.14	71	1613.71	341.53
9889	981.18	477.47	73	1620.07	396.24
15029	925.54	487.41	79	1688.81	378.2
6015	1123.82	384.91	78	1698.32	346
4330	991.16	483.62	84	1718.02	326.97
18909	1097.68	570.79	73	1735.42	607.51
3934	1109.15	552.14	74	1739.43	460.08
19363	867.12	620.13	74	1779.39	738.12
18002	1288.49	485.23	71	1800.22	448.73
4933	1364.86	630.42	74	1830.55	501.46
6380	1372.29	707.55	71	1841.36	514.23
16883	1363.62	527.7	78	2010.57	420.12
6072	1574.16	580.37	71	2013.52	377.64
17812	1417.56	569.56	70	2054.51	507.28
16701	1417.08	583.17	75	2071.93	447.2
6016	1345.93	620.12	75	2194.85	585.99
23261	1440.1	757.17	76	2245.13	579.05
9016	1484.15	791.38	72	2570.48	765.58
17524	1867.91	789.56	72	2578.07	684.86
22558	2228.15	660.37	73	3099.17	679.05
20502	2254.47	1019.37	72	3293.47	799.82

TABLE 3B: Hepatitis-inducing and NSAIDS				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1661	41.81	18.92	85%	1.48	29.99
16317	30.67	11.58	80%	8.6	15.46
11893	54.33	34.89	85%	10.78	84.99
1507	46.98	9	89%	15.22	15.58
22966	36.69	8.83	81%	19.74	17.28
19671	37.69	7.44	85%	22.27	14.65
20016	36	8.96	81%	22.47	17.54
18495	49.47	12.55	87%	26.89	16.39
671	1.28	14.77	83%	29.18	22.7
1221	443.26	150.05	94%	31.23	89.26
25938	56.45	7.66	83%	32.22	17.92
18389	86.77	18.28	87%	33.41	32.92
11974	-0.81	15.18	84%	37.19	30.74
15834	-27.94	45.21	80%	40.53	65.46
20161	128.51	48.18	89%	43.77	57.9
17809	73.73	16.32	83%	46.32	27.65
7056	3.07	13.95	81%	47.6	27.96
5384	140.18	41.23	89%	47.78	62.23
16809	124.52	30.87	89%	53.12	26.62
11423	97.3	21.17	90%	54.32	20.04
22918	25.37	5.71	92%	57.72	29.27
20354	223.3	84.74	94%	65.21	49.13
18529	131.4	33.67	86%	68.42	53.24
1514	90.15	14.51	83%	70.26	23.25
8079	-4.51	23.75	93%	71.3	43.24
23847	116.7	16.84	84%	72.04	35.87
9712	23.03	12.25	88%	77.04	28.42
3660	16.83	21.57	82%	79.66	62.38
11904	167.34	25.7	93%	81.27	36.83
19158	45.35	20.66	81%	83.61	36.03
3710	-36.33	22.78	94%	85.53	112.55
15207	201.4	59.51	87%	87.46	53.13
18272	60.07	14.42	82%	88.02	33.03
353	141.35	40.91	85%	91.87	108.42
19410	151.13	23.55	87%	95.16	23.41
22321	170.96	42.18	92%	100.6	89.13
17277	197.62	54.02	87%	107.61	40.04
8597	164.65	22.23	88%	114.16	40.18
22151	53.9	21.51	85%	114.65	59.1
8274	76.86	17.29	87%	123.17	47.02
6532	271.93	51.51	94%	134.9	41.19
21570	190.77	30.4	81%	139.02	39.64
2555	331.4	107.66	92%	140.78	56.13
25370	84.18	22.52	80%	142.29	76.05

TABLE 3B: Hepatitis-inducing and NSAIDS					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
14208	94.74	20.59	84%	147.42	57.13
4250	206.6	31.57	81%	151.25	44.71
1521	259.23	49.47	85%	156.72	61.63
19075	223.09	35.39	81%	163.86	101.01
23584	77.34	44.36	81%	169.97	88.21
23855	348.59	60.39	85%	174.64	78.04
9595	340.35	75.95	82%	175.69	67.44
13332	103.75	23.14	88%	187.8	61.54
10544	215.74	17.73	83%	188.96	55.01
20914	95.15	42	80%	195.52	132.48
1796	121.33	29.79	82%	209	97.51
21039	106.61	32.3	84%	211.38	102.32
18891	79.72	50.3	84%	246.65	190.37
5464	135.66	32.82	82%	247.44	149.05
15786	143.55	47.13	84%	247.54	88.85
22619	538.26	124.75	87%	252.1	119.33
2655	82.89	32.9	90%	258.6	179.08
12156	181.92	29.95	83%	278.7	159.97
17664	741.68	141.39	92%	307.07	186.68
3504	500.63	92.33	90%	315.63	104.18
21281	205.42	64.7	81%	330.89	91.63
23890	215.59	58.3	82%	335.94	112.79
21663	239	51.32	81%	340.75	88.67
1795	160.6	58.49	90%	341.81	148.58
6825	186.43	50.61	90%	343.11	120.89
1900	172.64	60.15	81%	346.3	165.46
18465	620.04	89.19	89%	351.76	235.3
19412	785.76	148.65	93%	362.14	121.09
4026	890.4	293.19	94%	365.48	125.1
9148	247.98	44.83	82%	370.2	91.6
12928	537.35	88.04	83%	411.28	98.02
2905	272.3	68.62	83%	428.13	203.06
21657	770.91	200.72	85%	465.93	129.71
15127	328.43	46.16	84%	473.84	141.3
20701	957.82	322.59	85%	491.66	156.52
23125	211.15	54.99	87%	522.67	517.03
15606	391.12	82.13	80%	555.3	143.44
13557	380.72	110.05	84%	601.18	180.33
3365	412.07	116.59	83%	652.4	245.48
18890	249.81	125.41	88%	681.61	362.92
21740	1634.89	574.14	94%	692.6	269.8
3121	283.35	133.91	89%	701.53	256.63
16458	914	77.34	87%	721.93	196.36
11720	1413.34	300.55	94%	727.31	251.26

TABLE 3B: Hepatitis-inducing and NSAIDS					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11504	489.83	118.52	82%	806.57	268.81
17768	607.41	128.96	82%	831.34	168.24
13093	311.95	133.36	85%	873.19	562.27
6236	496.56	151.3	84%	902.06	432.96
23449	168.69	130.37	84%	927.26	659.99
23989	1753.97	311.2	89%	1058.6	400.01
23448	180.53	167.78	84%	1073.75	757.46
24289	653.83	137.29	88%	1100.08	340.79
16885	781.13	224.04	92%	1490.2	403.55
3917	948.73	233.94	87%	1606.37	494.39
6072	1216.55	290.18	86%	1863.45	506.08
9016	1131.05	452.13	84%	2271.36	942.23
6189	1001.77	624.81	84%	2994.32	1665.75
16884	1730.22	430.96	83%	3305.32	4446.34

TABLE 3C: Necrosis and Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7271	47.32	123.63	82%	-98.96	40.35
1727	109.71	134.11	80%	-50.93	105.7
5780	186.95	173.5	86%	-46.09	31.81
13203	59.69	60.36	82%	-17.7	44.77
16513	26.79	31.17	82%	-17.26	20.41
14619	43.31	34.51	85%	2.15	12.76
4553	26.34	19.46	83%	3.22	9.94
13458	45.73	26.41	89%	5.65	18.85
1610	44.15	19.04	83%	12.68	16.79
14693	74.3	48.25	83%	13.17	17.15
23679	133.75	76.1	90%	13.54	19.85
20456	59.55	30.52	86%	15.2	27.25
5733	152.59	121.24	80%	16.96	49.09
23435	130.84	87.29	81%	21.19	45.23
15312	97.29	57.4	83%	23.69	24.18
23678	101.95	55.99	89%	23.69	13.19
15861	71.17	46.83	82%	24.47	42.1
9181	83.64	43.77	86%	24.64	15.48
1598	201.08	146.9	80%	25.42	45.83
19940	83.79	44.07	83%	25.73	17.82
9796	72.8	40.14	82%	25.76	21.99
16085	106.34	47.32	89%	28.48	22.62
13467	155.47	95.96	86%	30.98	34.92
16618	94.85	58.13	80%	33.73	25.67
24710	86.03	43.14	83%	33.9	21
23260	157.52	100.81	83%	37.65	37.29
22876	70.57	22.75	82%	37.66	16.34
9331	80.05	31.38	80%	38.03	18.65
12614	139.71	71.97	88%	39.91	23.39
3280	81.33	28.39	81%	40.1	20.81
13874	88.42	37.45	84%	40.85	22.09
15862	84.57	34.63	80%	42.44	41.06
5926	80.04	27.03	83%	42.65	20.36
20449	254.92	200.63	82%	44.06	38.62
15313	148.78	79.95	82%	44.12	32.74
2897	110.58	50.4	86%	47.14	25.32
10549	203.78	148.01	82%	49.51	39.18
7243	132.31	62.02	80%	50.65	27.72
14939	115.22	49.92	83%	53.09	45.97
14242	118.61	49.19	85%	53.41	25.56
7161	136.07	72.13	81%	53.54	28.94
20708	91.32	26.75	86%	53.6	18.5
3831	104.66	45.67	83%	54.97	24.3
21707	135.19	53.83	81%	55.69	51.38

TABLE 3C: Necrosis and Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
19264	117.33	44.24	83%	59.31	20.88
19150	109.31	32.72	86%	60.72	15.98
17687	99.1	21.62	85%	61.04	15.35
14462	156.22	62.83	84%	62.47	36.02
7036	131.87	57.57	81%	62.54	25.28
11527	177.9	80.35	84%	62.69	44.14
20082	124.7	51.02	84%	63.08	42.14
17736	432.83	313.35	81%	65.71	142.15
1841	136.63	50.08	81%	67.1	44.8
20523	102.48	38.3	83%	67.66	66.06
12965	169.8	78.23	83%	71.26	51.46
6085	208.53	104.4	83%	72.61	45.7
14458	330.83	217.41	83%	73.29	65.46
24236	184.01	75.75	85%	73.32	33.88
23160	176.55	75.81	83%	73.36	35.73
13251	323.03	180.5	84%	75.07	50.76
9784	153.22	64.68	82%	79.16	35.89
15398	239.17	147.09	84%	79.65	55.81
353	280.56	162.02	81%	80.59	90.86
20684	131.06	32.29	86%	86.62	20.64
14258	198.53	76.19	81%	87.06	38.11
22877	194.7	70.48	86%	93.61	36.71
1411	202.73	82.72	81%	98.83	39.17
11660	170.21	44.78	84%	99.62	34.3
23099	201.64	75.74	81%	104.62	41.86
23438	195.84	62.14	85%	104.93	43.18
17734	614.42	397.11	81%	110.47	174.81
7063	256.37	132.72	84%	114.31	69.93
1399	215.1	91.12	82%	116.84	76.67
5008	201.49	60.1	84%	118.38	36.13
11331	223.98	89.07	83%	120.5	40.92
25257	274.45	132.38	80%	121.28	48.13
16321	210.67	63.57	83%	124.13	43.97
20891	244.46	85.07	84%	125.01	52.71
2938	92.66	29.87	81%	127.24	29.13
22038	251.93	88.6	85%	127.34	44.31
17369	207.5	75.1	82%	129.13	60.27
5794	226.31	75.22	81%	130.44	40.81
5489	273.17	111.54	82%	136.39	59.55
20843	213.04	53.39	82%	136.57	33.06
2555	219.93	71.85	81%	139.38	59
15374	243.38	59.14	83%	141.32	44.16
24388	624.21	327.48	89%	143.82	68.72
22432	292.49	109.98	83%	146.05	50.66

TABLE 3C: Necrosis and Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18418	239.91	82.99	83%	146.58	40.53
12999	347.57	138.68	83%	153.73	65.66
26369	308.75	109.91	81%	154.12	55.73
14051	299.77	104	82%	156.87	52.25
4592	257.24	62.73	86%	157.37	38.03
4952	684.4	441.82	80%	158.99	145.89
23184	332.9	137.24	81%	159.3	52.72
7887	338.64	115.83	86%	162.05	60.73
18755	279.19	80.05	83%	163.56	53.86
17735	512.06	294.56	82%	167.32	151.69
4781	344.83	111.41	85%	169.37	65.78
22197	414.63	204.11	83%	169.48	88.02
23855	282.27	93.29	80%	171.07	75.56
14224	333.11	104.73	83%	174.8	67.56
6796	410.28	172.66	86%	185.7	72.52
20735	408.72	201.02	82%	185.89	74.3
21696	297.51	89.84	81%	186.09	42.02
11561	362.43	142.46	82%	188.78	64.86
3203	308.57	101.34	81%	194.76	46.19
7414	535.61	335.02	83%	197.35	92.11
15900	420.93	177.15	81%	202.45	80.18
23299	835.51	456.01	87%	214.06	131.12
2615	386.6	100.97	86%	217.6	65.98
5867	511.55	202.2	82%	233.57	78.63
24597	382.02	100.07	86%	233.91	54.34
11404	578.06	245.72	83%	238.77	146.51
1460	401.14	112.53	84%	244.96	91.82
498	416.48	120.92	83%	249.32	96.83
16859	472.45	162.72	81%	251.02	122.56
7888	537.76	182.29	85%	257.15	89.71
16756	553.61	229.09	83%	281.56	137.56
7064	502.34	176.81	85%	282.57	116.55
3418	612.35	201.12	86%	297.77	79.32
21458	1369.61	969.19	80%	306.95	224.17
2818	499.79	119.08	85%	321.5	81.64
23120	466.17	110.7	82%	322.94	76.21
4179	559.24	157.01	86%	323.2	127.86
21672	477.65	79.51	85%	327.31	77.78
23229	626.51	235.94	81%	338.12	95.94
1501	526.15	137.21	81%	342.01	115.25
7785	234.09	120.53	83%	402.39	211.3
6824	1330.86	651	84%	457.47	265.81
14962	735.07	188.78	85%	460.88	120.76
13646	647.84	120.93	81%	469.35	113.75

TABLE 3C: Necrosis and Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11693	194.51	110.15	81%	475.41	349.8
6132	303.54	124.75	81%	496.77	136.48
7935	319.95	130.18	81%	539.48	150.81
4193	471.49	196.67	86%	732.69	138.33
2569	363.05	288.34	84%	741.53	276.55
6143	440.17	239.99	82%	761.21	219.76
20503	406.67	194.67	86%	913.12	368.79
16703	657.32	260.25	82%	1074.26	319.63
7403	747.37	603.65	82%	1275.15	420.96
7199	888.57	501.29	81%	1460.27	432.28
15029	731.54	467.45	85%	1526.56	513.26
4330	744.46	374.66	83%	1547.62	486.62
6380	907.19	397.41	84%	1723.63	601.93
16883	1078.56	580.73	82%	1877.14	516.54
6016	1048.32	457.34	84%	2002.18	710.82
23261	1133.22	790.5	81%	2083.71	702.84
9016	1179.45	473.8	81%	2319.89	929.08

TABLE 3D: Necrosis With or Without Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
5780	149.44	174.82	83%	-46.61	31.66
14619	39.67	32.26	81%	1.81	12.49
5504	40.54	56.94	82%	4.45	12.06
13458	39.01	28.21	82%	5.58	18.92
15860	31.78	22.42	81%	6.3	24.49
14693	68.27	45.68	82%	12.72	16.78
23679	113.2	81.03	82%	13.37	19.88
15312	89.9	55.01	81%	23.16	23.77
15861	75.5	43.95	86%	23.4	41.45
9181	78.27	41.53	85%	24.18	14.99
16085	90.49	54.22	81%	28.58	22.73
13723	125.68	115.97	84%	29.26	45.67
23260	150.76	92.71	85%	36.36	35.87
9331	78.82	28.75	82%	37.48	18.21
12614	122.76	74.47	81%	39.76	23.36
13874	91.42	39.76	85%	39.87	20
15862	87.12	32.75	83%	41.59	40.71
2838	145.55	92.3	83%	42.77	33.6
15313	138.73	76.22	81%	43.33	32.1
2897	102.26	48.95	80%	46.84	25.34
10549	187.81	138.33	82%	48.44	38.17
14939	109.91	48.48	81%	52.56	45.94
14242	115.77	46.52	85%	52.64	24.7
17736	447.8	300.15	85%	58.86	128.94
19264	110.15	43.15	81%	59.01	20.79
14462	146.65	60.75	83%	61.81	35.78
15663	150.74	81.27	81%	61.88	28.94
13251	296.06	174.05	83%	73.46	48.79
6012	176.64	72.48	83%	84.55	40.71
22877	181.18	70.29	80%	93.15	36.67
1411	191.96	79.06	80%	98.12	38.82
11660	165	42.53	82%	98.96	34.06
17734	628.16	382.62	85%	101.62	156.16
6820	162.7	43.24	81%	105.26	24.87
1399	254.19	123.38	83%	112.16	66.1
7063	246.94	123.92	84%	112.9	69.1
24375	284.9	130.19	82%	122.22	50.94
22038	242.92	82.73	85%	126.16	43.47
15282	345.28	174.2	83%	133.39	77.83
20843	205.85	51.68	80%	135.98	32.8
11235	307.17	131.67	83%	138.32	42.12
15374	245.25	54.33	85%	139.6	42.14
8886	258.45	90.02	82%	140.07	40.87
24388	550.6	333.76	85%	142.43	67.72

TABLE 3D: Necrosis With or Without Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
6039	298.35	118.74	82%	149.78	54.28
26369	303.77	102.86	83%	152.16	53.29
14051	288.38	98.7	81%	155.61	51.3
4592	241.58	65.95	80%	157.11	38.16
17735	549.36	298.48	85%	159	133.2
7887	321.75	114.32	83%	160.72	59.56
18755	284.26	77.14	85%	161.37	50.75
4781	337.58	103.44	85%	167.27	63.76
20735	413.37	184.38	86%	182.1	67.45
7414	505.45	309.7	84%	194.61	89.53
11403	734.85	335.38	87%	196.39	177.82
15900	425.49	161.92	84%	198.73	74.48
15543	413.52	162.64	83%	212.02	73.08
23445	63.7	78.02	82%	213.22	89.74
6911	135.77	67.21	81%	214.68	51.49
11404	616.53	242.57	86%	230.44	130.03
5867	485.57	189.97	84%	231.42	77.22
1460	416.34	113.77	87%	241.33	86.89
7888	525.74	174.65	87%	253.82	84.82
26123	592.58	263.62	81%	267.76	130.29
16756	536.74	209.62	86%	278.76	136.63
24235	489.44	179.4	82%	280.21	94.54
3418	575.64	197.63	85%	295.93	78.26
19298	630.43	229.07	82%	317.49	143.34
23120	479.07	107.1	84%	319.7	71.63
2818	482.71	116.97	82%	320.15	81.06
15700	230.09	67.32	81%	324.4	64.93
228	236.54	61.87	80%	334.29	69.66
15032	205.99	56.82	80%	339.35	104.9
13294	644.35	170.98	82%	387.09	129.3
20707	228.73	113.6	81%	399.4	144.8
20299	283.13	98.83	81%	438.73	122.19
6824	1346.97	605.91	87%	442.76	235.61
14962	719.5	177.74	85%	457.94	118.72
794	301.18	105.82	81%	460.38	105.58
13646	650.4	113.01	84%	466.4	111.75
15135	628.19	146.12	81%	475.33	93.64
11693	181.61	105.42	82%	480.77	349.7
23390	900.94	286.52	82%	482.87	204.25
6132	287.11	119.69	84%	501.07	132.83
20705	268.91	129.82	81%	501.83	170.59
16518	745.69	208.61	80%	522.4	147.11
24501	924.14	324.29	81%	549.2	118.31
13684	940.24	251.12	84%	561.02	160.11

TABLE 3D: Necrosis With or Without Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23961	413.97	100.86	81%	563.48	84.42
2350	914.43	280.02	83%	566.27	157.14
7262	1171.93	460.29	82%	616.91	222.19
15283	1210.53	436.26	84%	630.12	224.34
4193	484.87	182.86	85%	735.61	136.93
15365	1249.48	437.43	82%	780.82	1098.83
24321	376.06	230.84	83%	789.46	268.88
22559	540.14	342.39	81%	1011.15	343.11
5899	694.24	374.16	80%	1263.41	404.09
7403	704.59	553.96	83%	1286.73	413.15
7199	835.65	469.87	84%	1473.34	421.86
15029	702.04	429.52	87%	1541.16	503.02
4330	675.9	370.63	85%	1565.51	467.91
18002	948.21	459.72	81%	1684.6	511.86
6380	882.65	369.95	86%	1738.14	594.45
16883	1007.86	547.7	85%	1895.14	498.99
6016	963.32	454.45	86%	2023.72	694.11
23261	1077.62	726.72	85%	2102.8	690.37
9016	1096.76	480.03	84%	2344.1	914.36
3062	1684.88	888.35	81%	2819.77	870.18

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
26190	48.28	140.35	73%	-116.76	71.12
8700	49.85	77.95	72%	-12.19	36.84
1661	36.36	40.61	72%	1.43	29.6
18323	56.4	33.89	74%	6.38	36.18
4348	50.39	34.87	73%	11.17	31.72
17481	36.46	27.96	72%	13.35	33.51
5434	29.26	14.26	76%	13.66	16.78
5930	23.92	9.03	70%	17.21	18.45
15778	24.37	10.62	70%	18.73	13.8
16251	28.52	7.89	78%	20.02	13.7
23315	33.84	16.8	71%	20.08	11.03
23843	65.54	53.1	73%	20.76	16.77
24268	31.94	6.01	72%	20.84	19.94
12185	40.45	26.74	73%	21.92	18.47
6026	60.83	27.25	80%	21.94	33.9
9603	38.75	22.25	71%	21.97	31.16
17747	8.38	6.53	74%	22.43	16.15
21799	-5.84	13.09	81%	23.01	22.31
14195	36.74	19.21	73%	23.09	19.24
3976	17.49	10.74	71%	23.34	30.4
6533	32.77	10.84	73%	23.83	29.19
9166	69.93	53.74	72%	26.99	17.75
4610	63.26	38.33	71%	31.07	36.11
16167	26.11	7.76	73%	34.04	13.5
13967	69.09	21.43	77%	35.02	22.23
17677	-27.82	68.69	74%	36.4	69.93
14449	56.08	25.32	70%	37.77	22.83
11700	55.37	19.55	71%	38.12	21.59
1538	7.74	23.48	75%	38.59	30.39
14053	24.71	9.07	76%	39.07	22.35
6804	17.85	7.18	72%	40.39	128.09
15834	-16.44	51.96	73%	40.56	65.53
23170	43.49	9.26	75%	40.79	23.99
21823	40.81	9.62	70%	41.44	26.15
11485	76.43	21.72	79%	41.78	31.48
26288	55.27	10.43	70%	42.31	15.42
25409	8.36	31.39	76%	43.05	24.65
15251	38.39	9.43	76%	46.23	24.25
8124	57.68	9.64	72%	46.93	19.16
14126	34.95	11.94	71%	47.89	50.38
25203	29.38	13.58	73%	47.94	21.85
9432	100.75	48.6	73%	48.25	28.18
2153	74.75	38.6	74%	49.01	17.57
11127	51.39	6.96	73%	50.24	17.35

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
2933	50.64	8.95	72%	51.06	22.58
25615	71.69	18.81	70%	52.1	17.72
24654	81.41	24.85	75%	52.19	24.88
15018	84.77	83.88	71%	52.26	40.53
21707	126.24	73.39	70%	59.01	53.51
13918	98.73	44.7	74%	59.06	31.3
10549	42.34	9.93	70%	59.31	64.81
22566	92.71	49.39	70%	60.91	42.33
23304	84.45	28.37	70%	61.03	41.36
25413	37.94	16.74	79%	61.59	20.66
25410	30.99	21.26	78%	62.85	30.41
25411	27.66	23.64	80%	62.98	33.69
13581	83.19	33.57	71%	63.07	26.31
13932	-7.5	82.93	71%	63.9	55.62
14171	74.42	21.1	71%	64.55	37.62
90	36.07	18.79	70%	65.79	40.02
17257	114.03	67.46	70%	67.08	34.52
7537	58.32	14.12	77%	67.47	33.14
25397	33.74	21.21	73%	68.15	31.21
17894	82.35	13.84	78%	68.79	26.36
6814	89.6	32.08	73%	69.88	23.93
21893	44.34	8.05	72%	71.05	72.75
11438	111.77	49.88	74%	71.31	27.16
23324	87.26	41.21	73%	73.64	76.07
4168	104.37	21.68	75%	75.31	30.27
7903	30.15	21.43	74%	75.81	76.12
14335	83.34	14.3	71%	76.03	33.52
24589	112.98	48.88	76%	76.16	48.86
9712	59.65	43.73	73%	76.42	28.63
20980	95.23	16.77	71%	79.04	22.6
6003	97.63	17.55	73%	80.11	26.51
13175	132.4	51.99	72%	81.55	39.28
19315	140.15	42.44	84%	81.73	41.23
15156	110.09	19.69	72%	81.74	31.08
1169	63.7	12.97	72%	82.79	31.48
6032	51.63	16.54	72%	83.57	48.94
17400	145.45	66.75	71%	85.87	52.06
2006	25.42	45.67	71%	86.52	90.27
21068	264.69	160.27	72%	87.31	146.99
11215	-7.35	163.64	72%	87.87	83.21
3074	54.49	18.32	70%	88.91	83.5
22961	111.83	20.67	72%	89.09	31.98
2506	141.66	97.88	71%	91.9	70.92
6409	148.77	36.6	74%	92.24	57.46

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22531	91.66	12.53	73%	93.27	36.37
21209	227.02	212.22	71%	95.2	92.15
2383	83.79	16.73	73%	102.14	37.31
11174	184.12	65.2	77%	102.16	98.46
17368	171.8	96.78	71%	103.87	47.72
20851	137.3	28.16	71%	104.02	55.43
3091	153.51	67.82	75%	104.92	90.83
18390	78.71	19.55	74%	106.46	50.88
3073	52.19	23.11	73%	106.62	118.05
6798	135.78	43.18	74%	106.64	46.11
14600	214.24	98.46	78%	109.92	74.91
17617	99.3	12.59	72%	110.02	31.44
14638	87.23	22.1	77%	111.45	74.07
10184	123.58	33.76	72%	112.37	55.43
9170	183.59	55.27	70%	114.2	52.72
22151	79.59	31.13	71%	114.31	59.46
12880	139.94	22.05	75%	114.56	32.47
14937	131.42	66.88	72%	114.75	41.55
2342	166.44	44.77	70%	115.31	58.59
18612	131.39	23.5	75%	116.94	56.6
11691	62.73	41.24	71%	118	79.85
17451	101.96	15.77	72%	120.36	30.67
19566	145.76	30.8	71%	120.45	44.75
24508	154.79	40.91	71%	123.72	32.09
1641	165.12	40.83	70%	128.2	35.55
23885	161.49	29.33	72%	129.48	47.42
20930	134.38	23.9	71%	130.09	61.62
5795	132.03	27.82	71%	130.17	53.46
22051	101.35	28.02	72%	130.68	67.38
26368	145.81	51.6	71%	132.19	91.73
19605	113.2	19.79	72%	133.82	51.82
21040	-18.07	52.54	71%	133.85	229.8
14776	102.58	34.94	70%	134.24	48.08
1223	182.79	51.88	71%	136.08	48.54
13762	158.63	98.43	77%	138.6	59.12
11048	119.54	22.24	73%	142.6	56.03
2292	84.06	42.12	70%	143.71	71.66
17844	277.9	176.64	73%	144.36	79.81
12215	204	107.83	71%	146.76	116.15
2043	179.12	22.45	78%	147.6	36.11
4157	177.19	33.3	74%	147.73	62.63
20711	228.01	78.2	72%	150.83	116.07
26088	145.54	50.27	74%	156.38	187.59
17572	159.65	44.25	71%	158.21	87.38

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1690	229.65	95.98	71%	160.28	60.57
15141	173.57	16.39	73%	162.21	36.81
16700	83.29	55.96	71%	162.48	108.7
20380	146.38	29.01	71%	163.02	57.5
15959	167.27	18.31	73%	166.48	70.66
9598	288.09	95.08	73%	168.1	93.9
11590	190.23	28.5	74%	168.24	68.73
22806	131.95	29.2	75%	169.43	77.82
18588	206.23	40.15	73%	170.98	65.63
1141	203.77	31.9	74%	172.68	35.21
9595	271.77	94.28	73%	176.57	69.08
24146	216.8	34.19	71%	177.31	65.74
17291	239.96	109.02	74%	177.33	137.8
21717	206.89	32.09	71%	189.62	69.87
13640	218.18	27.37	72%	190.6	71.83
14007	153.67	25.25	74%	191.38	72.77
16562	238.09	59.35	70%	194.57	50.93
10187	223.84	49.38	72%	198.22	88
25802	244.19	49.71	70%	214.98	65.34
11742	217.52	133.21	72%	216.12	86.16
5020	191.66	26.95	72%	222.98	53.97
22603	221.37	90.45	71%	229.9	65.5
1728	238.87	23.07	75%	230.92	67.51
13534	182.27	33.55	75%	232.74	85.78
2868	286.73	53.61	71%	234.2	69.67
14997	375.7	196	72%	235.84	152.48
5111	393.78	167.65	73%	236.27	143.66
20063	181.07	59.31	70%	236.39	97.14
16780	267.07	94.4	75%	242.2	64.47
23337	207.26	31.63	70%	243.84	91.24
19052	433.77	178.35	77%	253.21	91.88
22619	416.09	190.68	70%	253.69	121.24
6821	297.59	92.7	71%	255.52	167.53
17794	256.5	47.37	72%	259.54	87.89
5110	444.91	212.14	72%	270.46	106.82
4929	215.55	43.79	71%	270.62	101.5
23698	318.89	170.39	75%	278.46	123.55
10594	382.41	57.15	78%	291.69	58.26
6366	466.38	163.71	75%	301.16	141.67
5091	204.8	54.15	76%	305.72	121.65
12317	489.39	140.01	77%	306.86	86.66
15122	284.14	30.38	70%	308.23	65.78
2763	390	85.38	73%	308.26	88.64
20715	439.32	105.47	74%	310.12	180.07

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
25644	345.9	39.5	71%	314.7	121.98
1175	204.91	111.96	71%	321.32	143.78
24161	356.93	42.23	71%	327.71	79.09
18647	397.22	64.9	73%	330.24	91.79
21281	233.54	99.86	71%	330.78	91.46
4179	625.2	324.6	71%	330.92	127.34
43	237.61	86.82	75%	341.37	75.07
19458	364	43.15	72%	346.08	133.08
23128	313.06	51.91	71%	349.02	136.57
22412	366.89	96.19	71%	351.91	164.5
3143	483.63	141.06	72%	352.34	102.15
6801	355	56.71	70%	360.03	142.03
6066	431.59	75.6	72%	368.47	141.78
21575	432.67	63.41	73%	374.58	82.96
8317	421.43	158.85	72%	379.92	111.94
4371	507.88	124.44	71%	394.01	171.93
11157	373.15	134.06	70%	394.37	101.64
24296	481.18	92.3	72%	403.62	139.39
556	373.54	45.1	71%	408.23	71.6
13055	482.08	75.69	75%	411.9	164.09
8173	519.73	67.84	74%	419.47	110.06
3219	317.14	59.47	73%	426.13	99.03
16278	309.41	102.23	78%	429.92	164.15
23608	566.48	164.2	70%	431.27	241.18
25777	330.46	55.36	76%	441.54	130.73
18522	334.4	99.2	70%	443.31	151.76
6188	512.63	55.77	74%	448.02	139.04
794	333.35	131.81	72%	451.08	111.83
11693	254.85	149.73	72%	463	348.51
14312	397.8	81.06	71%	466.35	160.88
5339	852.55	606.3	72%	468.96	257.55
13646	546.37	100.3	71%	478.7	121.95
22534	444.69	49.89	76%	478.75	159.7
15121	635.12	147.29	73%	513.19	224.34
5038	398.62	86.39	71%	513.52	201.59
7916	483.75	53.88	76%	515.32	200.18
4759	421.47	104.72	71%	536.6	127.07
2339	519.32	64.43	73%	536.85	137.81
16947	444.15	113.82	74%	564.09	119.37
24707	469.06	76.22	77%	596.18	184.62
13557	472.83	125.45	74%	600	181.83
11322	781.82	176.95	71%	605.26	189.58
16623	815.06	113.69	75%	643.07	187.67
20397	756.19	106.73	71%	670.62	123.59

TABLE 3E: Protein Adduct Formers					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
3121	513.81	224.23	72%	698	260.45
6673	697.31	124.67	71%	713.3	302.28
4193	655.24	191.97	71%	718.19	154.45
7552	709.86	131.78	73%	813.29	320.57
820	636.5	127.73	71%	821.94	204.55
19105	924.47	159.69	70%	829.48	236.56
16169	456.68	219.61	72%	862.69	796.4
20503	559	204.67	80%	889.74	380.31
6236	529.47	148.78	79%	903.06	433.66
16879	841.82	418.27	71%	946.87	285.04
17340	1644.38	815.75	74%	997.68	474.22
7451	1340.55	383.41	73%	1014.34	341.2
12306	1456.43	258.06	79%	1024.68	517.58
18905	880.62	169.73	78%	1175.6	278.99
17027	844.61	248.1	71%	1257.61	538.33
22554	997.94	184.01	86%	1359.91	523.26
26147	1510.64	528.64	72%	1410.78	338.29
9192	941.24	221.51	74%	1413.17	565.76
23243	872.48	380.03	72%	1417.04	675.7
16885	1012.98	320.39	72%	1487.91	407.92
15029	1042.74	622.16	70%	1488.18	539.06
4330	1083.48	398.15	72%	1508.27	516.11
22266	1415.56	499.05	71%	1514.02	441.93
18002	1259.73	300.25	77%	1637.82	545.26
4933	1137.93	526.28	71%	1700.05	608.74
21091	1307.31	329.46	70%	1706.98	564.25
6072	1518.7	338.39	72%	1859.25	511.2
17812	1406.92	373.38	70%	1884.53	608.25
17107	1929.94	1307.4	71%	2218.38	823.7
9016	1497.78	482.54	71%	2267.81	949.1
20846	2090.67	1066.14	76%	2478.45	898.34
22558	2580.09	1019.35	72%	2867.4	846.53
6189	1470.69	763.08	73%	2992.11	1673.91
11623	2359.03	1401.37	73%	3039.92	2772.61
16884	1876.68	541.26	76%	3308.78	4455.6
6018	1795.01	783.44	73%	3626.1	3303

TABLE 3F: ANIT					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	633.15	232.37	98%	-132.38	329.17
19388	29.83	17.06	91%	-25.03	31.57
72	49.9	30.74	90%	-17.96	34.45
489	86.15	31.02	99%	-11.18	21.72
11645	46.52	22.15	95%	-10.46	29.11
15003	103.65	34.94	91%	5.13	35.34
4318	23.26	6.71	91%	7.08	9.22
372	43.1	11.62	90%	10.4	12.2
14400	115.49	28.78	96%	12.11	47.49
15480	45.43	16.54	92%	12.38	8.62
22397	98.15	29.08	90%	18.38	61.47
23679	58.03	21.94	92%	20.39	39.25
10790	-79.79	34.37	91%	24	51.35
16006	71.89	13.1	93%	26.66	31.65
15701	115.07	45.82	92%	29.52	22.06
25052	170.78	53.79	98%	31.24	82.74
1221	221.03	65.82	92%	36.47	104.6
23945	98.4	22.42	91%	37.09	29.06
11608	68.37	11.81	92%	39.75	16.9
20741	140.96	42.97	91%	47.33	36.73
5384	110.15	33.33	91%	48.7	63.05
1809	660.39	204.87	91%	51.86	210.98
21088	88.49	15.38	90%	52.62	15.58
488	302.77	84.83	99%	55.29	40.85
20708	69.43	8.17	90%	55.72	21.17
11940	79.89	7.9	90%	56.21	16.71
6585	124.92	40.67	93%	56.76	84.64
15914	167.68	28.59	98%	58.06	29.32
1279	124.99	36.23	92%	60.16	22.09
22487	203.14	70.64	92%	66.54	38.82
17894	123.11	19.61	91%	68.4	25.56
2801	158.72	27.08	95%	68.44	49.17
14465	5.28	16.66	90%	70.62	29.14
15892	279.1	77.25	95%	73.2	79.81
7903	9.08	6.85	90%	75.62	75.73
20772	127.51	24.47	94%	79.34	26.84
11904	152.49	15.73	96%	81.95	37.81
23522	149.93	28.04	91%	84.93	35.96
14017	168.86	47.57	91%	94.1	25.48
23869	219.91	36.9	95%	98.3	110.47
14016	172.79	34.4	91%	101.88	27.02
23005	231.25	60.04	96%	102.75	100.99
24453	296.76	77.39	97%	107.86	52.64
23872	208.24	51.83	93%	110.93	125.84

TABLE 3F: ANIT					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
10016	224.63	64.84	91%	116.67	48.65
17590	228.93	49.97	90%	127.17	38.31
4944	218.13	56.11	93%	129.57	134.8
15002	208.14	35.44	90%	134.25	36.07
20529	372.92	69.59	93%	138.52	121.65
20849	259.34	55.56	91%	150.94	38.19
15141	216.05	18.73	91%	161.78	36.17
15089	428.71	94.42	90%	164.31	111.52
24779	-119.55	53.79	90%	169.39	275.44
7665	325.89	51.47	94%	171.6	94
12577	530.07	99.18	92%	176.81	126.07
3253	242.21	21.26	92%	177.78	42.54
25069	384.72	63.15	96%	181.27	147.24
23182	70.96	27.02	90%	182.67	82.66
19043	461.37	93.08	91%	184.16	86.52
23445	44.92	13.64	96%	204.01	96.17
22928	18.25	13.42	90%	205.31	168.08
15300	301.52	31.01	95%	208.5	106.84
19073	357.79	55.66	90%	215.38	51.37
24237	602.69	44.81	99%	219.11	138.4
1447	293.32	18.87	94%	221.41	41.58
16408	151.08	35.06	90%	254.15	84.03
23868	529.77	129.48	90%	266.34	657.93
24810	103	36.24	90%	273.16	90.15
5235	460.06	75.16	90%	286.43	79.01
2802	498.79	58.22	95%	287.5	90.87
25747	698.21	163.03	91%	318.26	115.19
2818	510.22	88.82	94%	330.07	92.39
5934	42.22	26	94%	342.34	187.09
1501	711.93	121.22	96%	348.6	117.83
15535	499.6	40.24	91%	391.06	75.12
5437	327.15	25.07	90%	409.5	102.21
12928	607.12	43.69	97%	411.1	97.29
4207	611.82	98.48	90%	440.38	323.23
20701	762.37	110.98	94%	496.87	170.59
1562	360.31	37.96	90%	504.85	111.39
6824	806.51	180.29	90%	506.91	368.25
20983	343.07	66.3	93%	516.16	120.95
13088	199.67	54	96%	593.92	183.67
6613	320.2	65.66	92%	626.43	272.37
25024	451.39	46.56	91%	661.12	185.97
8549	262.14	62.15	93%	665.65	258.33
4193	484.74	47.1	95%	719.76	154.17
2569	257.19	110.15	91%	724.41	288.37

TABLE 3F: ANIT				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7892	1166.36	244.14	92%	809.73	244.53
18900	1202.22	137.08	92%	830.76	217.68
16879	540.35	100.54	93%	949.72	286.7
475	635.1	94.59	92%	976.05	230.62
5899	704.5	125.15	92%	1227.29	427.31
3916	883.71	181.1	91%	1427.83	464.67
10378	2563.09	466.04	90%	1469.47	449.7
19363	372.52	212.88	90%	1539.84	830.44
6072	1270.16	177.57	91%	1859.03	508.9
20502	1504.84	383.84	91%	3017.48	1038.48

TABLE 3G: Late Acetaminophen					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18028	62.86	12.89	98%	11.46	17.68
6151	41.98	5.06	97%	11.63	19.32
1394	46.55	7.94	98%	13.22	8.97
15701	104.85	30.26	98%	29.54	22.64
21586	129.12	22.29	98%	37.42	35.11
18099	74.54	10.03	98%	37.77	12.82
18990	191.58	50.21	98%	37.78	56
5492	154.99	36.3	98%	42.55	45.33
16958	152.1	24.97	99%	48.17	21.95
25892	5.84	14.89	97%	52.01	13.92
4281	8.04	4.69	97%	52.71	20.31
20817	552.74	204.49	99%	56.23	83.19
494	-58.87	15.28	99%	57.66	57
17091	221.12	37.22	99%	64.55	35.7
5493	201.07	32.69	98%	68.52	42.64
4650	257.12	41.99	98%	74.24	55.94
20818	387.65	157.18	99%	81.37	42.47
8356	191.89	39.3	98%	81.94	31.64
17090	166.91	23.91	98%	82.55	25.23
6153	47.01	7.23	98%	89.68	30.74
1399	422.27	102.52	97%	118.53	72.23
18369	14.78	33.12	98%	154.92	43.99
8107	82.52	12.58	99%	157.67	30.22
21305	78.03	11.47	97%	162.22	42.69
16219	91.23	10.22	97%	162.24	35.05
20380	51.46	16.74	97%	164.24	55.84
14970	64.35	7.2	98%	165.35	37.88
11039	22.92	14.76	98%	165.75	75.12
1644	69.04	14.22	99%	166.93	43.07
25632	23.75	9.64	100%	170.77	437.48
25069	648.62	107.28	98%	177.18	137.77
12848	77.84	12.22	98%	178.82	51.97
15571	37.5	7.71	100%	182.36	613.17
5998	82.64	16	98%	198.22	47.74
1542	75.63	15.75	97%	201.9	67.93
11429	113.75	15.07	97%	220.8	45.17
11635	84.37	10.31	100%	235.11	58.7
24246	680.67	154.62	97%	235.68	110.38
17684	115.68	11.83	97%	243.52	58.44
1479	111.19	13.1	98%	246.79	62.43
16023	118.74	16.82	97%	262.5	67.56
20986	100.65	16.03	98%	269.03	97.64
23033	164.75	20.5	97%	269.22	53.32
24810	78	27.42	97%	273.76	89.28

TABLE 3G: Late Acetaminophen					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8592	97.92	12.74	99%	275.69	78.69
12156	66.84	25.24	99%	279.94	158.15
20555	74.21	32.18	97%	280.75	96.14
18837	70.96	24.35	98%	281.18	112.85
17758	47.9	17.49	98%	283.74	151.83
11152	89.81	23.98	98%	284.55	88.62
22582	97.84	15.79	98%	290.41	88.62
6155	86.76	17.03	100%	302.82	149.97
10093	894.21	296.81	97%	307.41	125.35
23854	518.98	43.24	97%	317.71	83.8
4314	161.66	22.27	99%	325.66	70.88
20864	896.29	162.64	98%	340.85	169.02
9072	134.11	29.83	97%	372.6	132.4
15462	187.89	20.53	99%	377.51	69.64
3023	74.88	27.06	99%	377.75	123.14
1529	196.76	20.46	97%	378.11	72.49
24670	211.91	19.4	98%	380.22	75.72
25480	139.68	36.79	97%	384.92	88.4
4224	217.33	27.1	98%	385.39	68.02
1653	161.77	30.91	99%	413.84	133.06
9905	215.17	33.74	97%	417.78	81.53
11153	184.99	26.78	98%	424.64	112.76
21977	167.03	43.78	97%	425.7	100.74
21950	225.05	28.55	97%	431.25	83.14
2505	181.37	17.8	99%	437.97	99.3
794	185.22	23.41	98%	452.2	109.84
5920	1687.13	555.96	99%	456.93	241.47
2667	266.65	38.11	98%	472.54	95.54
24722	177.21	38.39	99%	491.55	112.03
23390	1178.14	133.27	98%	504.75	225.74
1562	261.12	32.84	98%	506.49	108.81
15113	155.11	52.14	98%	515.14	163.96
4199	289.55	26.97	98%	519.47	108.02
8872	1732.12	253.22	99%	539.58	281.13
24771	204.77	35.86	99%	548.56	123.7
13088	127.47	50.84	97%	595.53	180.73
17541	1185.11	145.34	98%	686.63	152.47
24811	244.05	55.21	98%	713.37	236.19
24321	133.15	53.97	98%	767.37	279.51
7552	180.78	39.85	98%	820.01	310.92
19732	145.53	28.91	98%	918.79	410.43
11205	330.78	77.32	97%	976.22	280.85
15673	1721.01	183.17	98%	1022.66	229.71
14512	230.44	36.6	99%	1088.1	390.72

TABLE 3G: Late Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11850	2429.93	244.48	98%	1189.68	370.45
633	647.11	128.95	97%	1346.47	304.28
14960	3443.82	469.79	99%	1352.48	446.55
22554	383.07	75.73	98%	1365.63	511.2
24049	4317.73	1756.71	97%	1441.54	440.22
2587	661.56	121.75	98%	1598.85	493.87
12314	743.43	156.24	98%	2014.22	647.46
15315	4723.83	784.41	97%	2482.27	635.01
17730	6017.72	1076.55	98%	2933.25	821.08
6189	422.42	136.09	97%	2994.06	1657.8
20873	5487.66	1292.77	97%	3014.46	6409.47

TABLE 3H: Early Acetominophen					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21175	8.2	4.71	94%	28.82	12.57
7528	8.32	4.93	95%	34.66	16.43
20282	-15.7	9.27	92%	36.02	33.93
5966	-2.42	11.53	95%	36.31	21.84
22695	10.13	6.89	92%	38.79	17.51
15634	1.39	5.65	94%	39.68	19.47
1520	15.99	5.3	94%	47.93	19.37
16524	20.02	6.63	94%	48.44	13.24
18482	16.24	5.44	95%	48.47	17.05
2280	19.83	5.96	93%	49.02	23.16
19787	15.18	6.28	94%	50.55	15.04
18584	6.53	10.13	95%	51.53	23.14
13926	21.46	6.96	92%	52.65	14.76
11423	15.02	8.15	94%	56.28	19.95
11940	21.79	9.2	93%	57.53	15.9
23000	22.53	12.08	93%	57.77	15.01
3080	-6.92	14.95	93%	58.31	48.7
23710	158.41	53.72	92%	58.38	71.02
23047	15.29	11.17	95%	58.49	16.56
16566	17.77	6.03	98%	58.51	15.69
19650	-70.3	47.02	93%	61.72	44.09
15467	11.36	7.01	95%	62.46	46.17
16728	14.72	12.75	92%	64.03	32.75
13568	28.12	10.02	94%	67.08	17.03
13932	-112.44	63.3	94%	67.38	48.47
15139	21.25	9.99	96%	68.11	25.84
24079	25.3	8.6	95%	69.08	26.17
22487	6.73	8.7	98%	70.08	41.42
14139	19.82	7.55	95%	71.65	22.54
15181	26.59	10.69	94%	79.78	30.61
23077	38.94	17.17	92%	81.22	21.14
17158	17.52	10.77	94%	83.01	45.36
20971	43.32	10.04	92%	83.29	21.37
1169	27.52	12.64	92%	83.96	30.23
16871	19.55	12.49	93%	85.46	26.85
9164	27.2	10.23	95%	85.81	27.4
15980	26.43	18.24	93%	86.7	23.87
16361	43.56	12.22	92%	91.15	25.64
21321	27.09	14.56	93%	105.32	56.02
3486	34.72	10.49	97%	107.9	41.25
2727	45.87	10.75	92%	110.53	48.76
8597	69.34	16.36	93%	116.43	40.21
574	65.57	6.51	93%	117.45	179.89
8730	45.4	17.81	92%	119.22	42.05

TABLE 3H: Early Acetominophen					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
13351	36.93	12.29	95%	122.54	50.81
6330	28.64	17.18	98%	123.06	58.01
18829	33.89	17.14	94%	128.07	58.85
16134	18.36	24.36	94%	128.31	40.65
20975	70.64	13.75	93%	135.77	31.44
64	64.42	13.23	93%	141.31	35.51
11426	36.73	16.99	94%	143.85	61.64
4127	42.82	25.2	92%	147.26	55.78
2043	94.32	14.17	93%	149.89	35.38
25814	49.58	15.47	93%	150.18	60.26
23044	256.5	54.33	94%	154.34	33.61
23491	80.29	14.78	92%	156.45	57.06
21909	77.01	15.95	92%	157.72	48.89
16364	54.12	18.74	92%	161.04	68.62
6861	53.34	24.76	95%	173.75	47.49
23709	365.56	102.97	92%	174.65	139.26
18981	80.53	12.18	98%	180	124.54
18136	92.28	22.73	96%	180.63	44.47
15170	63.67	31	93%	182.69	57.04
15491	50.3	18.75	94%	184.71	62.38
13640	81.51	25.5	94%	194.43	69.6
1542	110.94	15.7	93%	202.72	68.33
23711	965.1	437.75	93%	203.15	366.12
3549	100.08	20.01	93%	203.26	64.36
5749	105.17	17.76	96%	203.46	50.97
1921	469.15	75.54	94%	203.88	88.71
5953	1395.67	589.94	92%	204.16	203.2
11179	51.98	16.53	97%	213.56	68.01
17571	121.22	22.36	91%	215.28	47.28
1919	540.5	142.58	94%	224.99	91
16449	-17.52	49.15	92%	225.71	118.83
7927	58.81	47.71	94%	235.03	77.05
8735	104.51	40.55	92%	260.2	118.96
15070	64.72	20.64	92%	276.22	127.77
23606	645.68	142.54	92%	308.45	97.73
4291	55.74	33.3	95%	309.48	143.72
6366	132.6	38.47	93%	309.95	143.06
22862	102.99	68.89	92%	331.29	84.1
1920	699.35	125.66	94%	334.22	116.2
23230	101.11	53.57	94%	347.39	161.95
1802	68.01	68.24	93%	348.21	129.62
1501	135.65	55.72	93%	359.59	120.35
3143	180.22	37.55	93%	360.43	101.81
20799	195.78	28.73	95%	368.39	68.29

TABLE 3H: Early Acetominophen					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21980	205.1	26.69	96%	380.01	105.72
4234	728.11	88.4	91%	441.47	146.01
16215	277.82	31.3	92%	468.47	103.74
25705	303.85	36.79	95%	471.16	88.31
164	290.9	32.23	97%	476.12	84.6
21097	844.93	124.78	93%	521.05	142.52
23139	297.32	105.82	94%	614.3	226.46
8549	197.64	79.57	92%	674.01	251.68
9190	372.68	47.07	94%	1016.16	415.34
6291	552.9	84.63	97%	1091	307.85

TABLE 3I: Late Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17064	50.24	16.97	96%	-4.18	20
1625	114.41	34.24	99%	0.07	12.89
5885	38.36	18.29	97%	1.99	9.82
18046	46.73	12.92	99%	2.71	14.04
16649	220.02	92.9	99%	3.43	37.53
1554	47.01	20.46	98%	4.33	6.64
20950	54.4	13.02	98%	6.19	12
13458	58.51	18.25	97%	6.84	20.17
6879	53.86	20.46	98%	10.45	8.61
2065	77.67	43.56	98%	14.07	10.39
16654	153.26	64.25	99%	14.11	9.91
23651	330.28	228.17	97%	21.42	37.58
15312	116.71	36.41	96%	25.99	29.2
21818	119.6	30.36	97%	26.66	21.99
4048	1573.97	2042.27	100%	28.72	92.76
21695	174.77	50.28	99%	30.87	22.35
1126	93.96	18.28	98%	31.78	16.86
17157	116.08	34.36	98%	33.37	18.38
21586	155.13	41.01	98%	35.85	31.46
4097	202.62	143.18	96%	36.77	20.82
20589	204.58	80.85	99%	39.66	14.51
4856	195.72	58.45	98%	44.87	22.87
17500	1.65	7.49	96%	45.77	44.45
16730	154.98	38.01	97%	46.39	26.25
20449	440.43	164.04	98%	47.45	46.4
15655	237.45	149.71	98%	48.19	26.25
19040	396.02	114.12	99%	54.95	29.77
1037	191.13	61.49	99%	55.16	22.83
4178	263.2	73.51	99%	58.46	46.4
23302	134	32.72	97%	60.71	24.04
21060	195.49	44.63	99%	66.73	22.3
2781	300.75	90.51	100%	67.08	21.7
1571	306.34	84.06	98%	69.24	44.27
1258	201.18	53.89	99%	69.76	26.45
20755	315.54	99.4	98%	70.92	37.08
21416	180.67	33.54	98%	71.26	32.81
4327	209.63	44.69	97%	73.46	30.98
2853	243.76	74.49	99%	79.5	27.62
14458	462.45	169.29	97%	79.77	81.9
17956	135.44	24.53	96%	80.41	19.61
16650	335.98	95.22	99%	82.71	42.71
8152	184.75	44.1	98%	84.34	21.12
22321	565.88	166.7	98%	90.43	44.8
20801	244.26	53.66	97%	93.54	45.27

TABLE 3I: Late Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
15203	217.53	41.56	99%	94.08	22.2
16683	214.61	51.64	98%	96.97	26.38
7690	485.59	136.48	97%	98.07	100.2
18705	230.49	55.83	99%	103.84	19.16
574	566.67	151.26	99%	104.84	163.13
20644	284.09	69.38	96%	104.86	53.3
12613	385.02	81.17	98%	105.74	49.08
23173	527.13	156.81	99%	112.95	62.38
10016	305.83	117.64	98%	113.41	37.12
25257	401.37	69.21	98%	123.93	52.05
19377	245.39	39.45	98%	124.66	31.89
25313	368.62	55.36	99%	125.11	47.2
23888	323.47	71.72	99%	127.05	34.78
17754	280.21	65.27	98%	127.56	39.49
20891	284.25	57.73	96%	128.54	57.37
19241	305.11	61.55	99%	128.91	25.25
17369	251.93	28.1	96%	130.99	61.88
4049	1800.21	615.67	99%	131.28	173.33
4426	226.63	33.81	98%	134.21	26.79
15282	495.77	127.65	97%	140.76	88.42
20849	288.07	45.99	98%	148.97	33.86
17225	314.55	56.91	96%	156.73	51.3
24388	756.8	218.92	98%	158.69	122.1
16854	274.55	32.55	98%	161.83	29.13
16610	376.93	79.48	97%	165.18	49.27
6193	447.67	59.78	99%	194.57	54.15
3549	368.01	54.43	97%	196.19	60.45
2744	487.89	65.94	98%	202.98	55.42
15281	509.13	65.19	98%	207.9	69.15
17571	337.5	57.58	97%	209.52	44.91
8928	323.46	31.08	98%	210.05	36.77
25802	411.96	57.18	98%	210.79	57.41
12551	48.43	13.62	98%	212.69	71.68
7602	453.04	80.74	97%	213.06	62.29
15543	555.28	110.77	97%	219.06	83.33
958	492.73	90.77	98%	234.42	59.68
2854	520.08	129.87	99%	239.21	54.99
5331	517.46	66.57	99%	253.08	62.49
23013	631.62	255.14	98%	253.69	77.98
19768	497.6	88.61	97%	258.31	86.39
18107	475.79	86.06	98%	270.37	50.73
10306	537.72	79	97%	270.7	72.51
3138	773.53	129.57	99%	280.59	128.8
16684	591.01	105.06	98%	303.32	77.67

TABLE 3I: Late Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23854	563.93	104.51	97%	314.55	77.09
20897	602.65	120.81	96%	315.7	85.83
19298	835.39	188.74	97%	328.8	152.97
25718	579.2	77.87	98%	328.95	68.42
14959	676.74	116.99	97%	377.46	94.35
20879	73.93	55.35	98%	390.34	126.05
6824	1794.5	585.37	97%	479.02	298.25
13684	1052.78	207.71	96%	578.09	181.33
16438	1299.24	155.02	99%	582.93	144.92
4193	332.28	95.67	96%	726.26	144.3
7552	163.75	89.31	97%	826.93	304.52
16883	681.46	275.09	96%	1856.78	528.87

TABLE 3J: Early Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8663	721.93	225.97	97%	-87.65	146.96
8662	653.64	143.71	99%	-66.58	95.42
1727	348.89	185.42	95%	-57.26	75.16
11493	129.55	67.26	96%	-32.97	39.87
2628	251.75	147.92	96%	8.65	34
15647	109.5	26.81	94%	11.25	155.64
13265	78.29	37.64	97%	12.05	9.28
923	199.22	94.23	95%	15.81	23.49
8661	614.42	215.98	99%	16.84	60.47
7301	187.05	149.7	95%	19.02	15.94
15312	129.52	34.52	94%	23.98	24.69
1305	159.8	80	94%	27.12	24.91
1598	232.56	58.02	96%	28.01	58.64
23567	918.41	595.26	94%	30.79	97.73
25198	145.62	46.46	97%	31.18	21.37
22443	413.57	187.24	96%	32.31	38.97
809	170.72	83.79	94%	33	26.32
18043	157.01	66.2	95%	35.05	27.16
16825	86.21	14.87	95%	36.95	15.49
11494	365.78	87.61	98%	39.57	52.58
12969	315.69	145.09	97%	39.62	30.17
347	94.32	20.45	94%	44.31	19.5
15313	188.23	47.79	95%	44.81	34.49
25907	196.63	51.46	96%	45.95	29.69
2629	258.22	130.51	94%	47.27	31.18
4119	172.99	53.46	96%	49.1	27.57
15617	131.28	26.96	94%	49.13	28.01
11483	356.15	129.53	95%	49.85	57.22
25098	263.21	101.83	95%	51.71	35.09
8664	685.72	187.22	98%	51.77	117.57
7806	173.92	56.36	95%	51.78	24.26
5932	142.26	26.26	94%	51.91	24.37
18501	128.83	31.95	94%	53.7	17.47
352	306.66	117.09	94%	53.93	48.46
3831	120.45	24.02	95%	55.42	25.76
651	234.03	95.8	96%	55.88	31.26
650	252.68	84.65	96%	57.08	37.09
17337	140.87	38.01	95%	60.97	56.3
7036	176.78	42.65	98%	62.22	22.87
22124	125.04	23.89	94%	64.53	17.38
23587	208.43	60.7	94%	66.37	32.19
21130	369.23	131.33	98%	72.63	40.41
353	475.4	152.81	94%	76.96	69.6
1183	426.68	140.86	99%	78.14	33.96

TABLE 3J: Early Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
16080	464.2	128.58	94%	81.55	87.93
18349	210.66	61.07	98%	82.84	26.6
19184	623.72	284.24	97%	83.93	71.71
2788	214.08	67.37	95%	87.98	29.5
15291	225.71	67.73	96%	89.73	24.64
21380	195.27	36.2	95%	90.84	24.55
17908	489.98	67.94	99%	91.5	64.42
1475	764.62	270.51	94%	95.88	162.38
354	549.22	181.76	94%	96.35	76.24
14424	1887.85	604.98	95%	104.46	294.14
23438	233.78	45.73	94%	105.37	42.63
19085	235.47	46.91	96%	105.97	34.08
16318	569.79	137.14	98%	106.93	68.65
19641	354.6	119.72	94%	111.15	52.02
2049	351.74	96.17	96%	113.35	54.16
22625	588.59	137.7	98%	119.99	73.04
15616	363.79	100.12	94%	126.33	57.91
16081	590.52	148.03	94%	131.04	114.9
1306	354.57	112.94	96%	131.39	47.78
5489	361.63	79.95	96%	135.76	55.44
19086	312.97	47.23	96%	137.05	43.97
22681	1733.5	1045.76	94%	138.8	233.99
25567	440.46	120.5	94%	146.39	68.31
5820	392.73	112.42	94%	148.03	58.75
19075	541.95	182.12	95%	149.36	55.34
8314	4119.47	2769.99	98%	151.41	501.27
24234	520.49	130.96	97%	152.5	60.67
15490	337.2	71.58	94%	153.12	62.58
18259	558.61	152.63	96%	160.23	83.57
4952	867.67	202.68	94%	163.05	167.45
20795	498.26	84.68	97%	165.95	99.22
15292	331.21	64.99	94%	168.13	43.41
17735	616.97	206.23	95%	170.62	159.27
15382	2086.55	655.12	96%	179.06	342.56
6892	472.18	95.02	96%	185.03	58.03
10019	573.47	205.58	98%	186.54	69.46
8984	284.45	40.11	94%	186.61	41.02
3587	1589.64	832.55	95%	189.25	164.29
23331	343.71	75.44	96%	197.53	41.31
17753	422.58	107.22	94%	199.72	55.6
3430	482.45	99.02	96%	205.47	61.75
5937	398.98	79.16	95%	210.95	55.18
15091	457.85	75.14	94%	214.95	79.48
2615	475.24	65.04	95%	217.68	61.55

TABLE 3J: Early Carbon Tetrachloride					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22177	437.19	83.23	94%	220.99	76.02
15558	421.96	49.45	96%	261.21	89.18
15171	2476.94	637.89	99%	267.37	221.89
24235	651.38	135.2	94%	281.24	89.88
15172	1130.82	386.63	99%	294.17	160.06
8665	2451.27	808.98	94%	320.3	582.92
3816	941.08	189.07	97%	375.12	97.06
15051	1917.64	600.05	97%	421.84	274.9
6321	1227.19	294.21	96%	436.54	171.1
11495	1157.08	222.69	95%	479.89	170.9
19012	1131.9	195.46	95%	491.44	164.34
3139	3078.65	1586.03	96%	683.5	401.95

TABLE 3K: Late Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
25183	57.99	11.18	99%	-65.21	41.14
9969	66.32	43.47	97%	-28.99	30.94
19292	39.25	15.99	99%	-0.31	8.76
1749	36.95	4.96	97%	6.56	12.85
9697	56.57	15.67	98%	10.84	13.14
19465	72.95	28.72	97%	20.05	13.1
15441	57.11	16.22	98%	20.18	10.67
15987	363.79	45.36	100%	34.51	32.07
13580	0.18	7.99	96%	36.01	21.03
16319	89.11	16.96	97%	40.72	16.75
3510	7.29	10.94	97%	41.17	13.42
906	86.53	14.25	98%	49.56	12.1
19053	13.57	5.47	95%	50.36	50.88
5824	209.96	52.5	99%	54.58	27.78
17685	17.67	8.55	98%	59.93	29.82
4588	22.45	6.38	97%	60.62	24.09
14250	25.11	4.35	96%	61.29	33.6
17091	228.81	44.44	99%	65.14	36.75
4312	458.51	102.72	98%	74.88	65.39
6667	35.58	7.42	95%	79.42	27.4
9668	25.68	7.88	95%	82.74	43.74
17090	174.43	31.41	98%	82.84	25.5
14840	25.84	4.54	97%	84.25	56.66
18906	165.1	25.73	97%	86.57	33.68
21184	24.35	7.77	96%	88.84	44.65
11960	-21.76	29.8	98%	91.47	36.61
17092	282.98	55.61	99%	100.94	37.11
18316	41.41	4.56	96%	101.42	51.02
11724	26.29	6.1	97%	107.83	53.24
21238	29.51	14.62	96%	107.94	65.27
9015	50.88	4.22	97%	111.21	39.72
22204	31.75	11.16	96%	111.85	67.38
21228	60.32	10.12	95%	127.7	59.24
25725	303.56	97.38	99%	127.99	39.22
3381	215.51	15.65	98%	129.07	31.01
14199	49.89	11.18	96%	129.55	63.16
12158	539.59	79.37	98%	149.3	94.76
20711	15.4	13.95	97%	153.96	115.63
25055	543.96	83.34	98%	160.37	97.11
15955	401.03	64.61	97%	167.69	104.75
10002	79.22	8.3	96%	169.5	85.35
15888	103.8	7.37	96%	174.62	107.57
23709	91.99	7.53	96%	180.95	142.33
19255	96.69	11.59	96%	191.17	81.51

TABLE 3K: Late Cyproterone Acetate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
16124	59.91	18.31	97%	198.11	129.25
8053	55.5	21.16	95%	199.73	121.49
1796	713.84	124.8	99%	202.3	82.74
6431	44.99	10.12	99%	211.22	232.8
4576	60.8	23.4	95%	213.43	78.15
22713	83.58	18.05	96%	218.87	74.81
20803	489.88	37.25	100%	230.7	84.72
8905	129.45	13.33	96%	236.42	105.34
16780	482.97	115.87	98%	240.36	60.06
1479	143.4	14.02	96%	245.89	63.54
12156	947.53	169.32	98%	270.19	144.04
24860	762.67	137.57	99%	271.87	106.81
20744	131.35	9.57	96%	277.11	153.4
12157	890.46	241.3	96%	295.84	176.52
19256	169.36	16.84	97%	300.56	93.48
12155	849.1	121.68	98%	328.83	112.43
1795	886.32	169.03	98%	332.97	138.76
20864	838.11	192.14	98%	343.82	174.37
23032	174.66	35.02	96%	348.75	98.36
18860	658.47	93.14	97%	352.87	102.72
6801	167.82	26.32	95%	361.85	140
20915	707.08	113.27	95%	376.44	136.93
20707	836.46	117.26	98%	382.05	142.91
18473	830.53	86.28	99%	405.69	223.02
16278	872.29	116.7	98%	422.72	158.18
20041	189.58	32.85	98%	435.36	136.08
25056	1055.84	195.39	98%	435.67	129.34
20714	148.21	41.46	96%	438.15	637.41
15500	239.22	24.81	97%	456.63	119.52
15755	214.37	34.27	99%	457.32	99.49
11693	37.65	37.02	96%	462.5	345.74
15127	911.94	86.23	98%	466.74	134.84
21078	321.33	18.18	96%	470.87	98.57
19012	218.63	26.43	98%	519.87	206.37
20713	192.33	64.34	97%	523.9	200.74
8872	2206.69	222.08	99%	539.95	267.56
1551	300.22	24.52	98%	540.56	133.08
15391	748.88	48.29	98%	555.42	79.76
17541	1121.82	231.52	96%	689.41	156.88
2569	1283.55	169.03	96%	712.78	286.97
20804	2441.26	676.23	98%	723.52	393.32
12160	2592.66	403.1	99%	826.97	370.84
11644	421.94	97.8	96%	834	240.59
17788	2318.81	523.51	98%	909.78	263.72

TABLE 3K: Late Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17117	1568.35	191.58	96%	1006.34	230.44
15645	474.3	53.72	99%	1085.08	601.13
6479	446.51	75.83	98%	1215.32	472.08
22266	2441.41	319.93	97%	1502.46	434.41
21798	2671.47	378.77	98%	1532.27	351.77
1957	451.84	140.88	95%	1533.47	786.6

TABLE 3L: Early Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
12375	39.55	6.91	93%	6.16	21.17
2803	101.95	30.32	98%	12.74	30.67
18685	55.02	18.44	95%	16.95	33.49
15162	38.84	5.14	93%	19.37	14.99
10200	71.52	14.25	98%	21.52	18.12
11619	40.76	5.29	93%	24.39	9.81
5018	43.56	9.08	93%	25.12	11.36
11125	95.81	17.05	97%	28.28	20.68
25706	108.93	17.96	98%	28.74	24.94
17506	202.1	34.4	99%	28.98	70.24
25852	57.42	8.81	96%	29.52	10.16
16783	107.34	24.04	95%	33.35	33.97
4725	93.9	10.69	96%	40.84	123.37
15097	97.88	13.08	95%	42.76	28.79
2594	115.78	19.67	97%	43.16	28.35
18484	139.66	35.48	98%	43.46	17.72
7967	80.61	8.41	93%	45.01	25.09
15251	113.13	7.4	98%	45.58	23.44
14913	104.39	13.3	94%	51.71	28.53
15655	103.19	9.18	98%	52.4	44.96
5740	98.42	10.02	93%	54.17	22.49
15433	88.27	7.53	96%	55.12	26.88
6676	81.6	7.48	94%	55.36	26.6
12203	284.85	67.35	98%	57.37	50.59
11876	164.99	37.72	97%	59.91	38.15
24051	156.13	27.52	97%	60.29	28.94
24227	159.76	22.26	98%	64.47	29.99
23160	140.18	19.33	94%	79.22	46.25
24236	118.22	13	94%	79.8	46.11
5754	354.87	77.25	99%	82.05	52.7
5046	201.39	29.93	96%	91.8	52.22
4679	155.83	15.02	94%	93.09	39.05
2372	227.9	45.92	97%	99.62	37.53
466	147.74	16.09	93%	100.97	24.77
9128	497.34	121.83	99%	101.85	43.69
16087	72.43	6.68	96%	105.7	17.95
22898	203.84	9.33	98%	107.87	73.23
22717	160.84	13.59	94%	114.08	91.92
9775	472.31	82.29	98%	118.73	84.58
19605	335.27	35.78	99%	131.91	48.58
22503	297.45	72.36	96%	134.1	70.26
1903	323.28	80.7	97%	134.88	55.57
6582	298.97	43.04	96%	137.13	83.58
15030	175.94	7.66	94%	138.35	50.24

TABLE 3L: Early Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18235	287.07	66.63	97%	138.94	38.25
15282	203.3	21.11	94%	148.94	105
13799	391.75	74.97	99%	152.36	52.97
17955	257.17	57.57	93%	154.46	62.37
6272	415.31	82.23	98%	157.51	61.87
3266	238.25	22.7	93%	160.5	50.15
15959	389.2	63.99	97%	164.9	67.38
1884	191.9	7.86	93%	166.42	45.16
15955	294.4	26.85	95%	169.12	106.78
9486	468.68	91.29	94%	177.99	126.67
21275	349.64	80.81	96%	178.44	97.42
16053	311.13	32.05	96%	206.21	223.6
16747	445.78	87.8	96%	210.09	78.61
20350	393.34	72.05	94%	217.18	69.07
6855	290.54	8.31	95%	227.55	64.59
2326	437.32	39.57	98%	229.27	188.62
20063	579.31	78.7	98%	232.67	92.42
11403	386.09	85.89	93%	235.8	240.72
14303	381.51	38.02	94%	240.55	89.2
5696	167.33	17.35	93%	246.96	110.75
7586	568.83	104.54	95%	247.96	137.64
6821	667.02	106.37	96%	253.55	163
12956	525.48	76.44	96%	256.59	86.57
11404	487.51	32.83	97%	257.84	173.77
4092	428.51	31.72	96%	269.02	120.09
20	182.6	13.17	93%	280.26	77.1
7003	480.07	48.06	93%	299.91	136.85
22835	515.95	104.87	95%	316.8	87.86
22235	511.17	15.69	98%	321.64	119.46
1900	909.26	49.41	99%	339.05	159.22
9674	997.96	198.11	93%	345.29	332.5
2757	553.61	62.46	93%	349.8	112.21
3233	469.14	29.71	94%	350.16	111.19
4937	644.14	96.95	97%	351.09	99.81
16688	485.77	14.98	95%	367.52	115.86
8215	528.57	63.29	95%	395.11	169.02
23515	527.7	47.35	94%	399.57	182.28
22548	1110.25	157.18	97%	429.36	198.23
25056	701.5	107.45	94%	439.98	142.37
23030	298.12	25.05	94%	443.27	320.1
1930	795.75	79.48	96%	488.29	180.53
22379	987.52	105.4	98%	497.46	281.53
18280	625.22	42.6	95%	500.51	355.18
13557	431.55	35.49	94%	598.3	181.76

TABLE 3L: Early Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1901	1382.54	291.7	97%	621.54	268.35
16205	433.92	33.39	96%	622.45	128.79
19069	172.52	18.28	97%	622.95	345.06
22906	1189.14	110.88	96%	633	508.28
7262	974.62	93.19	94%	656.38	287.35
2354	1225.56	104.8	96%	666.98	252.59
7362	563.59	37.8	94%	816.77	299.68
15345	1802.55	235.04	95%	907.53	318.35
3803	1252.52	61.21	95%	914.67	209.78
22929	620.51	53.83	95%	1008.19	813.54

TABLE 3M: Late Diclofenac					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	2558.9	1121.55	99%	-137.91	262.53
19512	46.17	16.3	99%	-20.41	27.06
8700	150.91	57.74	98%	-11.7	37.23
19715	70.75	11.06	98%	-11.14	18.14
11645	79.3	16.37	99%	-10.24	29
20200	64.31	15.52	98%	-7.94	37.09
7858	64.65	32.07	99%	-1.01	21.41
22516	230.66	81.61	99%	0.06	50.52
18974	52.85	14.89	98%	1.86	14
5291	56.16	15.92	98%	7.46	12.49
9977	33.87	1.2	99%	9.6	16.15
372	53.19	3.15	99%	10.58	12.35
14400	168.71	36.04	98%	12.55	47.33
955	44.09	5.41	98%	13.21	12.09
26320	148.57	67.07	98%	20.83	30.04
23555	177.11	52.37	99%	22.61	21.13
10790	-147.58	11.69	99%	23.65	51
21445	152.54	38.45	99%	24.94	41.96
16173	102.32	21.29	99%	25.18	32.39
25052	653.33	363.97	98%	29.48	65.56
3452	158.59	24.76	99%	29.79	27.82
12277	126.55	32.95	98%	30.14	31.31
16240	-1.46	1.38	98%	31.65	28.31
22512	280.38	149.23	99%	44.34	59.45
7056	-11.07	4.54	99%	47.11	28.14
19411	117.91	13.87	98%	47.27	27.38
6198	184.84	21.67	99%	47.55	71.13
25246	17.4	2.21	98%	50.19	18.57
15504	223.77	86.68	98%	54.96	108.78
22514	404.55	221.07	99%	61.23	63.25
13045	-1.13	17.95	98%	64.8	29.82
9826	-2.67	5.61	99%	66.89	26.12
8079	-12.12	4.26	99%	70.37	43.83
2310	520.93	356.23	98%	71.67	85.7
25290	159.42	12.09	98%	74.09	78.6
1430	-67.02	9.22	98%	76.13	70.5
13895	199.32	16.84	98%	81.85	53.19
11904	162.22	8.31	98%	82.4	38.06
11596	208.15	21.91	98%	92.32	36.27
22515	1549.73	711.86	98%	100.85	133.92
22321	175.23	33.28	98%	101.48	89.03
8522	399.56	124.51	99%	108.85	69.48
14491	261.16	27.37	98%	115.78	52.28
21228	330.87	20.94	99%	125.87	57.45

TABLE 3M: Late Diclofenac					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
20529	887	406.86	98%	137.26	107.43
3250	366.5	30.94	99%	144.45	58.3
14504	691.37	422.61	99%	151.43	95.9
26133	549.15	106.67	98%	153.02	280.02
21978	81	5.94	98%	160.08	42.54
3708	397.54	42.39	98%	161.72	77.01
396	355.91	58.85	98%	172.48	57.78
23889	72.55	12	99%	175.14	49.66
12577	1097.35	411.24	98%	176.09	109.22
18580	822.77	189.24	98%	201.23	172.81
24237	928.14	321.39	98%	219.99	132.72
25618	180.02	2.6	98%	245.62	81.24
4969	1833.13	949.96	98%	265.19	240.61
5110	738.94	147.68	98%	271.77	107.36
25619	193.88	2.98	98%	274.38	108.29
13353	101.42	6.77	99%	275.78	68.9
7225	610.95	103.39	98%	276.52	112.14
1175	89.72	12.52	98%	319.98	143.49
4314	199.22	16.19	98%	324.04	72.64
21281	119	14.89	99%	329.77	91.62
699	744.08	166.35	98%	385.87	84.98
17281	191.29	11.48	99%	407.86	108.78
7697	126.05	9.16	99%	418.46	147.54
24012	650.52	28.61	99%	423.59	476.52
5339	1561.45	746.53	98%	471.48	259.27
1561	1103.42	310.4	98%	483.63	109.78
24228	1037.63	336.37	98%	510.12	105.18
5616	1252.37	399.53	98%	617.19	131.84
15189	2393.48	562.64	98%	642.89	398.85
563	1286.12	293.65	98%	647.49	154.22
19392	1380.71	448.01	98%	669.42	123.39
21740	2258.4	588.09	98%	701.14	280.06
1854	2250.76	618.07	99%	730.54	265.59
3292	2871.21	931.15	99%	892.15	311.65
22598	2831.24	966.7	98%	1051.05	357.55
21661	2797.22	982.49	98%	1087.36	376.19
21660	4837.56	1684.22	98%	1692.71	582.02
17167	4555.27	1157.69	98%	2481.92	715.65

TABLE 3N: Early Diclofenac					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
10667	411.83	248.79	97%	13.74	165.12
17695	47.26	305.83	96%	15.36	60.09
3452	91.31	23.32	97%	29.73	28.67
21421	5.58	8.51	95%	31.49	16.56
6222	-12.72	9.64	95%	32.02	30.46
14996	180.85	117.09	98%	32.69	45.29
12844	-11.84	8.74	96%	39.54	27.67
1843	88.96	20.57	96%	48.67	17.77
9635	-9.83	19.06	95%	48.68	40.62
21707	169.82	64.58	95%	59.13	53.37
23302	37.52	28.79	96%	62.8	26.58
13932	-63.25	79.49	95%	63.9	55.2
18604	24.17	7.4	97%	65.08	25.49
20354	220.66	86.86	98%	66.15	50.9
1841	188.63	53.81	95%	69.83	46.13
355	149.37	52.24	97%	71.24	34.86
17683	40.01	12.49	96%	77.75	25.92
2359	17.87	8.17	98%	86.55	44.73
3713	168.44	419.14	97%	89.98	96.34
11840	51.82	10.03	96%	100.7	37.97
19211	88.71	85.04	96%	108.71	56.23
17800	70.19	39.86	98%	118.7	28.58
1844	277.5	69.37	96%	129.25	44.39
356	249.59	82.38	98%	129.82	46.84
23494	49.03	10.06	96%	131.42	50.45
14776	49.01	22.62	97%	134.61	47.31
23626	251.41	69.01	97%	141.32	90.59
23491	85.95	100.32	96%	155.17	56.53
21382	60.1	10.48	95%	162.86	70.74
6213	75.91	24.03	97%	177.43	53.8
15170	66.01	17.61	95%	180.78	58.76
23182	47.61	14.34	95%	182.97	82.24
14958	77.51	24.88	99%	192.52	57.74
16562	315.91	84.36	96%	194	49.14
23043	116.23	50.3	97%	200.45	58.35
18996	115.11	26.79	96%	211.48	69.45
14997	807.1	529.54	98%	231.67	129.71
10879	84.17	41	95%	235.09	83.29
11021	90.03	69.2	95%	247.67	106.37
2655	43.2	16.5	97%	258.1	178.54
16859	704.09	252.4	97%	258.84	124.37
17794	130.88	63.44	97%	261.13	86.21
6919	1235.49	468.87	99%	269.17	229.63
13353	151.45	114.9	97%	276.39	67.85

TABLE 3N: Early Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
20	432.75	81.44	97%	277.59	75.26
12964	106.32	33.26	95%	288.44	95.46
3722	585.01	101.14	97%	295.66	101.48
20715	308.31	50.21	96%	313.11	180.79
23606	668.08	172.75	97%	313.49	105.76
23230	176.98	99.78	98%	342.52	164.69
12946	142.18	31.13	97%	349.51	100.28
24200	1265.26	395.08	97%	369.8	208.75
16768	264.62	55.65	95%	376.13	78.38
12857	231.61	293.1	96%	392.81	143.31
18795	726.51	149.33	97%	395.27	107.88
19	654.92	135.45	97%	397.11	105.29
18783	716.54	157.61	95%	402.03	119.63
19252	288.39	79.84	95%	410.59	104.1
1114	645.09	101.99	96%	427.86	137.39
20698	914.65	381.61	97%	479.92	178.44
21098	1119.71	394.89	99%	521.35	157.69
21097	883.9	345.03	98%	525.66	142.61
15191	1868.16	232.88	99%	528.3	355.46
19373	957.63	171.61	96%	529.59	254.13
9424	1020	141.63	96%	537.58	150.22
15606	331.04	100.93	95%	555.14	142.5
4670	2609.57	936.24	97%	576.03	466.99
402	1115.89	448.86	99%	596.85	131.13
13557	267.85	27.9	96%	601.37	178.89
2368	429.73	38.72	96%	606.25	88.63
22906	2134.54	974.52	97%	617.58	470.92
15189	1986.69	445.74	98%	635.58	391.8
15190	2159.12	392.22	99%	661.42	378.72
1995	1259.5	439.49	98%	684.23	244.32
11830	1983.61	566.45	98%	692.89	304.27
1805	1229.6	164.21	97%	703.35	218.45
1174	1340.59	440.4	96%	726.33	411.01
6013	1139.77	436.67	96%	749.39	184.56
17785	1846.83	672.05	97%	752.99	445.33
22840	1352.3	529.97	95%	755.78	273.45
8515	346.51	83	96%	765.99	292.49
21574	391.95	100	97%	817.75	226.02
6477	1367.6	542.86	97%	857.33	304.69
3292	1879.44	784.97	98%	890.76	323.1
12306	3293.83	1170.7	99%	1005.26	433.69
7451	1583.77	483.79	96%	1014.48	337.6
6295	2775.87	1040.34	99%	1068.45	493.12
21467	2391.61	1040.88	96%	1118.01	516.67

TABLE 3N: Early Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
6633	2355.01	832.32	99%	1206.88	312.71
14738	2426.79	883.37	99%	1231.22	312.92
3730	2978.69	1180.6	98%	1232.87	586.1
3617	2869.63	1011.46	98%	1268.73	398.2
8715	3069.61	1101.03	99%	1353.63	759.44
17672	2889.9	351.84	96%	1930.21	397.38
26152	5392.56	2027.73	98%	1991.62	852.89
20846	4030.03	570.84	96%	2449.47	889.44
6018	11859.37	4320.03	98%	3477.55	3126.6

TABLE 3O: Estradiol					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
19476	221.25	108.8	94%	-58.59	73.88
20579	65.59	26.23	87%	-13.8	30.61
4520	74.3	35.09	90%	-1.56	34.15
55	34.69	14.89	86%	4.7	13.41
384	44.98	13.2	86%	5.76	28.49
22722	566.51	262.91	96%	19.66	47.88
12120	291.19	164.4	93%	20.32	48.27
16283	59.56	11.97	91%	25.04	15.43
10611	78.35	19.48	91%	26.01	28.58
3570	1203.99	486.89	96%	27.26	139.67
3929	66.1	15.81	88%	32.04	17.87
16783	94.16	35.66	86%	32.29	33.01
6604	9.87	7.84	88%	36.24	17.57
10540	70.62	15.26	85%	39.69	19.11
3846	63.36	11.22	85%	40.64	15.95
14266	463.56	161.4	95%	42	79.9
15097	-4.06	20.79	88%	44.39	28.23
16809	77.26	7.57	89%	53.84	28.46
672	185.2	45.2	92%	57.01	48.59
25290	322.26	83.7	94%	68.08	67.25
5493	104.13	22.09	86%	69.51	45.42
17699	379.25	121.82	95%	77.01	64.08
15057	178.76	62.35	89%	80.64	61.88
4082	137.71	29.22	87%	81.24	39.54
3074	305.3	91.43	94%	82.44	74.5
12655	222.74	65.14	88%	90.1	61.41
3073	404.03	113.1	94%	97.56	106.47
23220	158.44	34.05	86%	104.71	23.6
18612	214.55	48.01	88%	114.72	54.02
24442	253.1	51.52	95%	119.28	39.27
19258	345.84	102.07	91%	119.63	94.13
6789	266.72	63.61	88%	130.61	57.1
11465	687.63	230.97	94%	136.61	114.55
23491	259.04	44.02	89%	151.54	55.44
3075	515.63	145.3	94%	159.61	267.05
19261	291.37	82.45	86%	163.74	57.85
17393	223.13	34.27	86%	164.98	67.02
23987	254.16	41.43	86%	168.68	53.84
13229	314.84	68.95	90%	184.84	61.96
15295	252.4	28.26	85%	191.1	52.8
23183	91.05	26.84	85%	192.16	88.8
6549	522.38	151.13	89%	204.39	114.46
13092	440.75	124.27	92%	206.68	86.61
9402	278.52	27.55	85%	207.63	69.5

TABLE 3O: Estradiol					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23362	362.98	58.85	92%	209.03	55.26
729	141.14	32.05	85%	209.19	55.66
13963	572.36	193.21	91%	220.12	112.51
17516	287.34	30.47	85%	223.48	56.14
7927	368.05	56.64	86%	226.41	79.19
14989	306.39	34.48	90%	229.8	59.41
5464	608.63	139.88	93%	235.86	136.35
14997	313.77	45.38	92%	237.05	156.21
23337	388.86	61.57	87%	239.19	87.95
6541	835.22	410.07	90%	240.86	107.93
9621	349.89	41.41	91%	242.89	62.26
18877	1770.96	536.63	95%	251.02	323.54
19825	76.2	82.83	85%	256.34	107.9
291	413.96	84.34	85%	256.37	66.6
17613	349.67	47.08	86%	259.18	106.99
19824	83.21	81.92	87%	260.01	99.57
7684	577.91	188.77	85%	279.08	126.11
2373	634.92	150.17	92%	285.8	133.51
2484	57.67	44.88	86%	289.53	213.13
16684	447.2	65.17	88%	306.67	87.7
6975	700.83	228.78	86%	312.49	161.5
18141	1086.32	372.55	88%	330.82	216.89
25718	464.33	56.04	91%	331.59	76.26
18742	172.88	37.74	87%	352.25	190.08
12361	1014.46	256.68	94%	354.09	232.49
16327	558.02	61.36	88%	369.06	94.06
21164	169.42	47.37	86%	370.17	185.53
24012	2053.62	525.68	94%	382.21	392.09
4674	167.98	66.36	88%	452.2	224.88
6060	310.86	53.86	86%	477.05	121.08
1561	310.14	86.6	90%	491.78	117.97
11227	841.6	140.02	86%	496.07	212.99
19728	229.27	93.53	88%	501.97	174.65
12746	759.81	83.64	93%	520.3	104.48
12585	909.57	150.85	86%	542.79	178.84
23437	271.75	62.16	86%	558.17	246.21
11821	1051.26	228.29	86%	574.09	309.97
24707	407.68	85.92	85%	598.16	183.22
16894	1105.64	177.51	91%	731.2	332.55
11720	397.65	148.44	88%	748.93	265
4440	398.17	156.94	89%	804.73	210.24
7584	2336.91	636.07	91%	819.41	712.46
13093	2287.36	766.73	90%	825.52	505.38
11644	485.11	142.46	86%	838.95	238.55

TABLE 3O: Estradiol					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
9475	422.84	219.9	86%	958.81	372.8
24112	1879.78	259.59	90%	1026.22	630.45
16703	714.02	96.32	86%	1057.6	331.01
15534	1418.23	154.26	88%	1104.88	261.78
14738	862.34	156.54	85%	1256.55	349.62
14960	1831.5	294.22	85%	1370.37	509.8
22554	609.46	270.71	86%	1371.14	511.54
6015	707.01	273.93	89%	1539.98	455.17
7497	1136.4	136.44	87%	1691.66	329.88

TABLE 3P: Late Indomethacin					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21075	56.56	18.08	99%	-101.64	72.06
3626	270.02	126.67	99%	-91.68	41.85
20522	88.79	62.74	99%	-86.26	44.12
18203	28.03	7.89	100%	-59.65	26.67
21682	139.83	65.11	99%	-56.8	31.49
20119	75.13	51.9	99%	-51.89	22.95
945	164.01	44.63	98%	-32.43	36.01
8017	40.5	7.12	99%	-4.91	18.36
22516	427.71	48.74	100%	-3.53	27.61
7858	133.46	131.64	99%	-2.18	10.32
11731	57.13	15.61	99%	-1.13	13.51
2011	88.53	22.86	99%	5.7	10.46
19121	104.23	50.09	99%	16.77	12.76
24826	218.27	46.71	99%	17.2	179.73
23555	133.19	49.37	99%	22.23	20.8
21445	313.48	71.78	99%	22.36	29.24
1777	117.77	21.2	99%	22.67	16.4
16173	249.12	60.67	99%	23.05	21.76
21683	179.43	48.48	99%	24.37	26.58
19503	106.66	42.52	99%	24.54	12.74
19444	479	225.49	99%	26.17	29.3
20651	252.93	78.27	99%	26.84	24.52
11172	108.09	14.64	99%	27.38	25.08
7196	70.2	6.99	99%	27.5	18.37
8864	168.51	38.98	98%	28.16	40.98
25052	413.35	149.76	98%	28.65	72.19
12277	188.8	30.97	99%	28.87	27.27
20134	115.79	25.97	99%	31.07	21.72
15961	155.48	44.33	99%	31.59	27.65
22897	135.13	41.74	99%	33.43	19.08
1893	250.46	53.73	99%	40.37	21.42
22512	493.75	186.61	99%	40.54	35.84
14081	1307.16	578.37	99%	40.73	109.27
25083	96.77	17.16	99%	41.1	19.54
17500	182.9	29.18	100%	43.12	42.04
2013	191.84	31.9	99%	44.55	23.34
8273	410.92	194.88	99%	45.89	30.96
19411	184.69	32.53	99%	46.1	23.55
15504	896.04	321.22	99%	46.28	53.42
22514	543.21	150.84	99%	57.67	44.72
155	187.91	27.8	99%	62.07	21.49
20523	337.44	89.8	98%	66.71	58.22
16961	225.29	41.42	99%	71.58	40.53
24589	412.43	149.59	98%	73.14	30.15

TABLE 3P: Late Indomethacin					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21285	903.94	338.62	99%	73.28	108.74
15503	519.54	109.49	100%	74.61	27.28
6200	1572.18	522.18	99%	78	145.78
7743	288.96	85.4	98%	83.77	52.71
2012	357.34	70.02	99%	84.87	34.39
3749	-48.1	12.54	99%	87.36	48.17
4892	2121.77	1018.81	99%	97.96	339.86
24651	168.51	30.23	98%	98.36	20.05
23005	536.62	86.56	99%	99.43	90.49
1700	273.11	39.16	99%	102.11	30.56
22898	507.42	174.82	99%	103.97	57.4
8522	552.47	146.35	99%	105.43	54.02
12714	0.7	18.22	98%	106.47	34.92
15116	243.85	52.64	98%	107.4	25.94
17277	239.1	35.46	99%	107.78	39.78
22042	21.05	10.38	98%	109.25	91.56
21414	1412.18	189.99	99%	116.04	143.33
17258	235.7	32.66	99%	120.39	25.05
682	555.72	137.48	99%	126.28	58.1
17369	441.37	64.2	99%	130.38	54.83
20529	790.13	186.87	99%	134.07	101.45
14504	773.65	116.14	99%	147.38	84.22
154	347.17	63.6	99%	154.37	37.49
12450	-60.33	24.42	99%	154.48	84.94
6431	1828.3	421.64	99%	190.99	149.33
18580	1167.73	411.76	99%	193.7	141.11
8310	107.35	13.86	99%	204.96	44.79
14330	633.28	126.05	99%	225.12	77.1
5687	48.78	22.59	99%	227.66	79.73
14185	760.34	170.85	99%	253.08	93.43
21443	569.4	110.65	99%	256.7	61.78
16519	807.19	191.58	98%	273.02	117.31
9079	820.52	184.52	98%	316.54	112.19
19469	162.04	26.75	99%	325.82	57.22
373	115.43	31.34	99%	334.03	85.91
43	156.53	22.34	99%	341.11	74.71
20864	37.65	12.15	100%	352.3	179.09
699	762.57	112.9	99%	383.6	79.72
24323	230.34	24.71	99%	398.78	95.09
17281	100.34	30.42	99%	410.15	105.21
16366	113.72	34.12	99%	439.22	103.99
21014	188.22	42.97	99%	572.37	137.02
16367	166.59	86.34	99%	612.27	144.06
25525	264.07	72.58	99%	645.12	117.62

TABLE 3P: Late Indomethacin					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
635	308.38	68.87	99%	672.17	126.74
18890	126.36	42.96	99%	679.93	361.87
634	355.69	72.95	99%	705.77	125.16
6236	227.28	73.91	98%	902.24	429.28
10984	135.85	78.66	99%	1092.48	362.92
15029	181.72	50.19	99%	1492.95	529.6
4933	357.28	114.44	99%	1702.56	598.89

TABLE 3Q: Early Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21682	85.12	87.03	93%	-56.37	33.66
1510	75.53	7.54	96%	-13.1	65.66
26280	109.21	31.74	89%	-10.05	85.78
11422	60.74	22.85	91%	13.75	11.38
1507	46.96	9.51	87%	15.4	15.74
16251	34.42	5.87	90%	20.02	13.62
19671	39.81	7.46	90%	22.33	14.64
23106	48.6	11.99	93%	28.28	33.85
2736	49.82	5.14	93%	29.89	18.47
25077	111.99	30.35	88%	30.69	73.6
1221	445.47	178.19	92%	33.57	94.3
18389	94.31	16.02	94%	33.62	32.95
3972	-24.58	15.09	94%	34.18	35.89
18237	63.23	7.16	91%	36.35	20.91
22725	4.84	8.57	88%	36.54	24.3
17854	94.21	22.12	90%	48.6	21.13
25379	64.97	7.1	91%	48.71	16.47
1843	85.73	19.01	94%	48.71	17.88
4504	96.84	28.13	90%	48.77	77.49
24024	75.74	15.08	90%	50.05	33.85
16809	117.87	32.17	90%	53.62	27.39
11423	102.73	23.05	89%	54.5	20.13
2042	92.88	5.97	96%	54.98	50.98
13992	110.02	45.53	90%	55.81	24.86
22918	27.24	5.2	92%	57.51	29.32
5059	222.71	98.2	92%	61.9	61.99
20354	194.32	79.46	91%	66.49	51.97
18529	139.38	36.52	88%	68.68	53.21
8079	-1.13	28.24	91%	70.82	43.57
7176	83.8	6.04	89%	71.68	21.23
24721	116.01	17.12	91%	75.35	29.71
11904	169.62	30.75	91%	81.73	37.23
3710	-40.52	24.79	89%	84.89	112.56
1271	127.09	19.36	88%	87.87	22.54
15207	207.84	67.65	90%	88.03	53.57
21256	150.53	29.3	87%	90.66	43.12
1572	134.45	17.05	87%	92.3	26.58
19410	154.21	25.11	89%	95.44	23.68
16080	172.16	50.03	89%	95.77	117.15
17950	134.99	16.51	87%	96.23	39.64
22321	169.07	47.34	95%	101.03	89.08
9223	166.07	27.83	88%	106.75	43.32
17277	186.86	45.28	88%	108.27	41.12
16125	212.34	60.78	90%	109.55	34.54

TABLE 3Q: Early Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
354	156.92	39.75	88%	113.78	121.78
22151	49.94	21.66	90%	114.35	59.07
16477	205.91	47.02	87%	118.16	42.37
15884	197.78	19.66	96%	119.51	58.67
25768	189	17.68	94%	128.02	30.12
6532	275.04	58.08	92%	135.65	42.31
2555	342.38	116.88	91%	141.73	57.69
25370	95.55	12.34	87%	141.81	76.1
1426	186.05	11.71	91%	141.89	28.02
16081	293.29	79.31	90%	147.43	146.68
154	240.39	32.25	90%	155.47	42.04
1521	271.17	53.27	87%	157.16	61.75
22806	82.54	19.97	89%	169.69	77.1
1141	221.49	23.61	89%	172.77	35.13
9595	369.54	72.63	90%	176.26	67.68
21709	240.64	11.92	95%	179.9	33.86
13332	111.82	16.97	88%	187.21	61.88
21444	292.61	40.73	91%	204.56	58.9
20350	333.21	45.66	91%	216.95	69.67
3776	316.54	58.6	88%	226.04	54.29
958	283.88	16	89%	240.09	72.64
18891	63.95	40.8	91%	245.89	190.12
15786	130.41	48.25	89%	247.11	88.8
22619	509.69	128.09	87%	254.11	122.09
2655	76.89	36.89	90%	257.67	178.99
21443	408.93	75.59	90%	258.32	68.58
17664	718.76	159.35	90%	309.86	189.82
1795	179.95	54.13	87%	340.51	149.15
6825	188.01	57.66	89%	342.19	121.17
18465	583.12	68.3	93%	353.78	236.17
19412	798.48	156.59	91%	364.41	124.75
4026	854.17	324.83	92%	368.96	133.71
20915	208.25	51.68	88%	381.94	139.96
12463	631.37	114.76	89%	391.56	105.49
7122	778.65	154.65	89%	421.1	129.61
23245	695.04	100.61	88%	453.5	126.98
20701	818.5	138.91	89%	496.14	169.1
23125	203.3	56.02	88%	520.99	516.04
21740	1357.78	289.81	91%	701.6	296.47
16458	933.78	80.79	89%	722.78	196.14
11720	1393.76	333.85	92%	731.5	257.06
23449	166.05	104.49	89%	922.94	660.67
23989	1702.06	285.92	87%	1063.27	404.32
22368	637.02	202.48	88%	1081.65	343.44

TABLE 3Q: Early Indomethacin					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
24289	672.7	120.08	88%	1097.27	342.03
16885	837.41	195.77	91%	1485.4	407.68
9267	809.11	323.93	92%	1667.39	543.29

TABLE 3R: Valproate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
26190	239.04	44.21	99%	-115.53	71.46
2154	26.52	22.45	98%	-34	15.98
12625	129.76	35.25	98%	-7.97	79.74
4231	160.07	13.84	100%	-6.47	34.51
360	42.77	15.77	97%	-5.58	16.63
24126	127.21	24.22	97%	6.68	31.59
8993	64.31	7.77	99%	8.92	10.71
19762	168.43	71.93	99%	9.69	24.52
11336	60.09	15.29	99%	12.42	10.72
20993	73.86	17.79	98%	12.51	23.49
330	76.9	11.84	98%	13.5	26.03
12058	48.89	5.96	98%	16.85	15.53
1579	75.5	19.78	98%	16.86	13.09
5993	49.43	5.91	97%	17.56	13.02
8054	63.83	11.7	97%	17.56	15.18
23315	53.08	6.14	98%	20.16	11.05
23843	102.85	21.92	99%	21.2	18.22
11315	170.88	30.14	98%	22.9	42.27
13812	138.26	33.46	99%	26.62	22.64
23106	97.66	12.04	99%	28.05	33.33
11625	70.95	9.83	97%	28.43	16.22
9374	155.52	11.78	99%	30.44	41.52
10394	210.39	57.19	99%	35.12	29.91
6101	146.33	49.53	97%	38.17	25.87
2117	107.64	17.82	97%	43.75	19.24
12614	113.54	14.75	98%	45.51	37.01
9766	130.53	51.66	98%	47.22	33.17
2932	256.87	86.84	98%	48.26	30.66
13501	145.64	35.69	98%	48.87	22.87
14913	145.2	21.59	98%	51.42	27.75
16673	133.08	23.07	98%	53.6	21.07
2042	183.57	50.07	98%	54.55	49.7
2915	150.2	35.95	98%	55.29	23.13
19669	192.83	28.28	99%	60.25	31.79
19264	145.96	13.12	98%	62.26	25.95
17257	197.58	17.21	99%	67.22	34.6
15663	157.22	12.55	98%	67.92	42.04
11527	186.56	12.56	97%	68.89	53.83
22375	201.22	32.17	99%	75.66	28.1
5754	289.15	110.18	98%	82.52	54.48
12198	157.09	5.38	99%	83.53	37.27
18885	179.92	14.06	99%	85.54	27.13
13166	392.55	98.9	98%	89.27	56.47
13251	155.07	11.85	97%	89.73	88.96

TABLE 3R: Valproate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8728	346.01	114.17	98%	90.12	40.25
2216	234.47	28.59	99%	94.87	37.16
21535	197.23	12.53	98%	96.15	38.42
21567	509.19	66.46	98%	97.9	104.57
10593	328.02	63.73	99%	101.91	43.97
17368	241.72	37.58	97%	104.44	49.02
9800	366.46	11.6	99%	105.66	68.67
17479	261.87	40.08	99%	106.14	33.44
21976	256.5	24.3	98%	106.4	45.51
14600	242.39	40.76	98%	111.36	76.44
22570	241.74	26.13	97%	111.56	44.08
23656	273.7	31.03	98%	112.56	52.23
15179	255.98	37.97	98%	112.9	41.1
16616	304.19	58.02	98%	115.37	49.86
5608	233.3	11.25	97%	122.33	53.28
20090	263.76	45.31	98%	126.59	32.66
17644	333.21	52.99	98%	128.35	68.07
15149	345.13	64.29	97%	128.59	59.92
6789	283.91	53.49	99%	133.02	59.87
6686	369.2	41.65	99%	139.06	46.36
19230	391.37	57.35	98%	149.61	84.83
13949	47.22	6.84	99%	151.24	58.29
11280	287.5	36.75	98%	159.37	38.65
19513	345.16	59.75	97%	163.49	60.93
23762	321.28	26.82	97%	164.97	66.22
13838	437.29	30.14	99%	166.7	55.87
2691	316.24	12.09	98%	168.14	70.13
9572	409.53	66.85	99%	168.33	60.29
6861	397.87	34.78	100%	168.71	47.4
22135	361.16	95.89	98%	170.63	47.21
24388	283.3	44.23	98%	172.33	155.38
18886	403.05	74.14	98%	175.49	63.14
24368	602.67	63.22	99%	183.22	79.82
5381	356.13	13.85	99%	191.57	49.01
9402	342.47	21.74	97%	208.49	68.96
17261	546.81	71.98	99%	219.95	72.35
2101	430.5	35.07	99%	224.81	67.09
24369	546.78	56.44	97%	228.98	103.39
11354	530	66.53	99%	229.49	68.24
8709	90.79	24.72	98%	233.09	61.98
24367	400.74	12.79	99%	245.59	55.58
19052	646.73	83.13	98%	254.53	92.68
22957	665.35	87.82	98%	274.44	208.86
15551	493.87	26.61	99%	304.36	63.07

TABLE 3R: Valproate					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
12317	639.88	73.89	99%	308.65	88.02
4179	845.91	78.29	98%	333.97	135.14
6440	961.78	166.32	97%	351.53	186.44
7111	553.56	43.59	98%	353.19	75.73
18285	707.67	76.76	99%	357.46	132.75
12928	791.23	86.89	98%	410.91	94.08
15051	1110.61	136.73	97%	476.75	412.42
2569	338.95	14.84	98%	721.15	290.78
3803	499.92	74.41	97%	920.04	208.7
18962	573.38	98.13	99%	1606.33	624.84
5052	906.23	65.55	99%	1930.67	442.76
22540	1108.89	178.44	97%	2311.11	657.83

TABLE 3S: WY-14643					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
3175	81.67	38.5	98%	-24.57	20
2051	31.61	16.91	98%	-19.67	25.77
23627	40.97	4.93	98%	-14.82	37.36
16409	95.86	23.34	97%	-8.25	35.38
14116	38.83	17.55	99%	-7.83	5.25
18029	208.84	94.33	98%	-7.23	21.53
6677	32.1	15.65	98%	-6.62	9.95
20856	275.88	94.5	99%	-5.26	14.41
5565	221.64	85.1	97%	17.46	47.37
12467	216.39	65.04	99%	20.32	20.78
23500	148.59	59.24	99%	22.05	17.54
1858	529	114.56	99%	23.94	68.23
8820	81.06	9.86	99%	28.61	31.53
18082	128.62	31.47	99%	29.7	16.97
4931	135.4	29.63	97%	33.8	32.95
9925	117.26	29.18	98%	42.43	17
24381	97.68	12.7	98%	43.65	17.97
6292	96.5	10.27	98%	43.76	16.97
5518	-34.55	15.68	100%	44.56	14.44
18083	370.91	74.26	98%	45.23	60.06
4272	590.58	82.76	100%	47.77	61.51
7295	114.22	11.36	98%	48.54	27.07
8315	251.82	52.39	98%	50.52	44.35
20855	205.89	56.89	100%	51.41	13.97
15018	153.93	12.99	97%	51.69	40.82
22046	173.79	36.81	97%	52.05	35.05
4438	-53.05	31.71	99%	53.83	12.81
18956	233.24	49.47	99%	57.47	28.38
3631	135.16	24.43	97%	62.18	23.06
4271	1146.85	102.6	100%	63.33	94.28
6553	215.81	43.91	97%	64.81	42.7
3558	192.81	32.74	98%	65.12	31.67
20038	306.38	66.25	98%	68.41	50.76
7517	190.58	26.66	98%	71.67	32.59
3743	185.35	31.74	99%	71.95	25.24
14507	291.71	54.52	98%	74.57	66.85
18749	288.03	90.54	98%	77.94	40.13
4290	293.68	45.21	98%	87.32	46.32
14595	321.16	55.3	98%	89.33	56.57
14264	331.35	82.51	98%	91.8	58.3
397	232.66	39.79	99%	91.99	32.22
18746	280.52	43.35	98%	93.45	48.78
3439	244.57	26.7	99%	100.37	28.67
2190	164.79	17.03	97%	100.78	189.02

TABLE 3S: WY-14643					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18318	279.93	40.82	98%	111.57	48.48
5887	1076.32	275.73	99%	111.64	138.98
3513	212.58	33.36	98%	114.18	27.84
22416	1001.99	170.33	99%	121.52	83.97
22224	487.47	76.85	99%	124.54	72.09
12215	632.99	209.38	98%	141.79	100.45
9373	419.3	49.02	98%	144.86	76.23
15672	378.23	65.03	98%	151.17	68.05
3260	508.28	175.97	98%	153.29	72.65
16700	596.39	103.44	99%	155.05	96.4
18747	457.04	82.08	97%	155.98	76.29
26109	1286.05	121.59	99%	156.58	201.4
22737	685.5	206.71	99%	168.28	96.83
3720	315.08	30.72	98%	179.69	49.62
2113	410.43	34.36	99%	185.32	58.03
15015	374.26	31.51	99%	192.11	63.36
6439	425.56	74.96	97%	196.56	74.01
22370	945.85	62.98	100%	216.15	108.38
2457	1132.75	158.6	99%	227.31	140.2
1728	477.23	66.78	98%	227.92	60.65
18891	1245.42	225.38	99%	230.61	151.12
22620	386.56	21.42	98%	235.22	68.77
19591	567.11	40.94	99%	237.04	108.52
5602	1404.36	215.76	99%	242.82	212.8
24860	67.15	34.2	97%	279.45	115.83
22392	598.76	55.66	99%	296.04	67.51
18742	1303.27	263.5	99%	335.32	154.05
6825	626.39	47.06	98%	336.52	118
21164	991.37	155.11	99%	356.95	172.12
9372	1244.96	107.3	99%	368.29	225.64
8177	121.78	23.64	97%	389.45	423.88
17935	1404.15	220.52	97%	416.54	273.3
10533	1054.36	147.32	98%	421.36	212.4
16944	747.42	72.2	98%	422.41	133.98
21354	2186.83	317.02	98%	437.51	348.77
16323	223.57	44.79	99%	465.4	220.36
9423	273.32	30.42	98%	486.76	134.12
19044	814.58	45.86	97%	502.31	184.58
18727	206.23	25.52	99%	516.82	179.53
18125	1062.51	80.83	99%	529.14	174.32
16704	1486.63	221.63	97%	565.52	242.61
3099	922.46	83.44	97%	599.33	119.33
2813	1250.39	172.69	98%	603.02	185.25
20998	325.2	72.5	97%	606.04	134.27

TABLE 3S: WY-14643					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21010	1699.76	218.74	98%	606.25	249.41
14882	377.63	34.39	97%	607.89	168.14
5616	386.99	47.15	97%	623.82	140.57
16945	1098.96	98.19	98%	628.67	192.67
7420	1415.94	79.85	97%	655.69	311.93
18890	1900.82	258.12	99%	657.78	337.82
3279	1571.19	374.24	98%	708.13	199.08
16190	1581.05	206.33	98%	716.2	226.42
20597	378.94	48.6	98%	742.21	189.37
21341	1797.23	203.99	98%	768.53	328.94
4940	623.22	140.4	98%	1632.44	469.8

WE CLAIM:

1. A method of predicting at least one toxic effect of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of at least one toxic effect.

2. A method of predicting the progression of a toxic effect of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of toxicity progression.

3. A method of predicting the hepatotoxicity of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of hepatotoxicity.

4. A method of identifying an agent that modulates the onset or progression of a toxic response, comprising:

(a) exposing a cell to the agent and a known toxin; and

(b) detecting the expression level of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of toxicity.

5. A method of predicting the cellular pathways that a compound modulates in a cell, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is associated the modulation of at least one cellular pathway.

6. The method of any one of claims 1-5, wherein the expression levels of at least 3 genes are detected.

7. The method of any one of claims 1-5, wherein the expression levels of at least 4 genes are detected.

8. The method of any one of claims 1-5, wherein the expression levels of at least 5 genes are detected.

9. The method of any one of claims 1-5, wherein the expression levels of at least 6 genes are detected.

10. The method of any one of claims 1-5, wherein the expression levels of at least 7 genes are detected.

11. The method of any one of claims 1-5, wherein the expression levels of at least 8 genes are detected.

12. The method of any one of claims 1-5, wherein the expression levels of at least 9 genes are detected.

13. The method of any one of claims 1-5, wherein the expression levels of at least 10 genes are detected.

14. A method of claim 1 or 2, wherein the effect is selected from the group consisting of hepatitis, liver necrosis, protein adduct formation and fatty liver.

15. A method of claim 3, wherein the hepatotoxicity is associated with at least one liver disease pathology selected from the group consisting of hepatitis, liver necrosis, protein adduct formation and fatty liver.

16. A method of claim 5, wherein the cellular pathway is modulated by a toxin selected from the group consisting of amitryptiline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

17. A set of at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-3.

18. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 3 genes.

19. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 5 genes.

20. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 7 genes.

21. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 10 genes.

22. A set of probes according to any one of claims 17-21, wherein the probes are attached to a solid support.

23. A set of probes according to claim 22, wherein the solid support is selected from the group consisting of a membrane, a glass support and a silicon support.

24. A solid support comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-3.

25. A solid support of claim 24, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.

26. A solid support of claim 25, wherein the array comprises at least 100 different oligonucleotides in discrete locations per square centimeter.

27. A solid support of claim 25, wherein the array comprises at least 1000 different oligonucleotides in discrete locations per square centimeter.

28. A solid support of claim 25, wherein the array comprises at least 10,000 different oligonucleotides in discrete locations per square centimeter.

29. A computer system comprising:

(a) a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes in Tables 1-3; and

(b) a user interface to view the information.

30. A computer system of claim 29, wherein the database further comprises sequence information for the genes.

31. A computer system of claim 29, wherein the database further comprises information identifying the expression level for the set of genes in the tissue or cell sample before exposure to a hepatotoxin.

32. A computer system of claim 29, wherein the database further comprises information identifying the expression level of the set of genes in a tissue or cell sample exposed to at least a second hepatotoxin.

33. A computer system of any of claims 29-32, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

34. A computer system of claim 33, wherein the external database is GenBank.

35. A method of using a computer system of any one of claims 29-32 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 1-3, comprising:

(a) comparing the expression level of at least one gene in Tables 1-3 in a tissue or cell exposed to a test agent to the level of expression of the gene in the database.

36. A method of claim 35, wherein the expression levels of at least two genes are compared.

37. A method of claim 35, wherein the expression levels of at least five genes are compared.

38. A method of claim 35, wherein the expression levels of at least ten genes are compared.

39. A method of claim 35, further comprising the step of displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level when exposed to a toxin.

40. A method of claim 4, wherein the known toxin is a hepatotoxin.

41. A method of claim 37, wherein the hepatotoxin is selected from the group consisting of ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

42. A method of any one of claims 1-5, wherein nearly all of the genes in Tables 1-3 are detected.

43. A method of claim 42, wherein all of the genes in any one of Tables 3A-3S are detected.

44. A kit comprising at least one solid support of any one of claims 24-28 packaged with gene expression information for said genes.

45. A kit of claim 44, wherein the gene expression information comprises gene expression levels in a tissue or cell sample exposed to a hepatotoxin.

46. A kit of claim 45, wherein the gene expression information is in an electronic format.

47. A method of any one of claims 1-5, wherein the compound exposure is *in vivo* or *in vitro*.

48. A method of any one of claims 1-5, wherein the level of expression is detected by an amplification or hybridization assay.

49. A method of claim 48, wherein the amplification assay is quantitative or semi-quantitative PCR.

50 A method of claim 48, wherein the hybridization assay is selected from the group consisting of Northern blot, dot or slot blot, nuclease protection and microarray assays.

51. A method of identifying an agent that modulates at least one activity of a protein encoded by a gene in Tables 1-3 comprising:

(a) exposing the protein to the agent; and

(b) assaying at least one activity of said protein.

52. A method of claim 51 wherein the agent is exposed to a cell expressing the protein.

53. A method of claim 52 wherein the cell is exposed to a known toxin.

54. A method of claim 53 wherein the toxin modulates the expression of the protein.

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60/297,457	13 June 2001 (13.06.2001)	US
60/298,884	19 June 2001 (19.06.2001)	US
60/303,459	9 July 2001 (09.07.2001)	US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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14 August 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/010453 A3

(54) Title: MOLECULAR TOXICOLOGY MODELING

(57) Abstract: The present invention is based on the elucidation of the global changes in gene expression and the identification of toxicity markers in tissues or cells exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The invention includes a database of genes characterized by toxin-induced differential expression that is designed for use with microarrays and other solid-phase probes.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/23872

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68 G06F19/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	RABURN DOUGLAS J ET AL: "Stage-specific expression of B cell translocation gene 1 in rat testis." ENDOCRINOLOGY, vol. 136, no. 12, 1995, pages 5769-5777, XP002219695 ISSN: 0013-7227 page 5570, left-hand column, paragraph 4 figure 1	17, 22-24, 44-46
Y		1-4,14, 15,40, 41,47-50
X	-& DATABASE GENBANK 'Online! NCBI26 January 1996 (1996-01-26) RABURN ET AL.: "Rattus norvegicus anti-proliferative factor (BTG1) mRNA" retrieved from HTTP://WWW.NCBI.NLM.NIH.GOV Database accession no. L26268 XP002219696	17, 22-24, 44-46
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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
20 November 2002	21.03.03

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Ulbrecht, M

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
	the whole document	
Y		1-4,14, 15,40, 41,47-50

X	BISSIG MARCO ET AL: "Functional Expression Cloning of the Canalicular Sulfate Transport System of Rat Hepatocytes" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 269, no. 4, 28 January 1994 (1994-01-28), pages 3017-3021, XP002190711 ISSN: 0021-9258 figure 6	17, 22-24, 44-46
Y		1-4,14, 15,40, 41,47-50
X	-& DATABASE GENBANK 'Online! NCBI12 April 1994 (1994-04-12) BISSIG ET AL.: "Rattus norvegicus sulfate anion-transporter (sat-1) mRNA" retrieved from HTTP://WWW.NCBI.NLM.NIH.GOV Database accession no. L23413 XP002219697 the whole document	17, 22-24, 44-46
Y		1-4,14, 15,40, 41,47-50

Y	WO 00 12760 A (INCYTE PHARMA INC ;SEILHAMER JEFFREY J (US); PANZER SCOTT R (US);) 9 March 2000 (2000-03-09) page 2, line 11 -page 3, line 25 page 26, line 16 -page 30, line 30 tables 1-9 claim 1	1-4,14, 15,40, 41,47-50

Y	FARR S ET AL: "CONCISE REVIEW: GENE EXPRESSION APPLIED TO TOXICOLOGY" TOXICOLOGICAL SCIENCES, ACADEMIC PRESS, SAN DIEGO, FL,, US, vol. 50, no. 1, July 1999 (1999-07), pages 1-9, XP001096475 ISSN: 1096-6080 page 1, right-hand column, paragraph 2 -page 3, right-hand column, paragraph 2	1-4,14, 15,40, 41,47-50

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/23872

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
Y	NUWAYSIR E F ET AL: "MICROARRAYS AND TOXICOLOGY: THE ADVENT OF TOXICOGENOMICS" MOLECULAR CARCINOGENESIS, ALAN LISS, NEW YORK, NY,, US, vol. 24, no. 3, March 1999 (1999-03), pages 153-159, XP001008421 ISSN: 0899-1987 page 153, right-hand column, paragraph 2 -page 157, right-hand column, paragraph 1	1-4,14, 15,40, 41,47-50

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/23872

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: 29-39
because they relate to subject matter not required to be searched by this Authority, namely:

Rule 39.1(v) PCT - Presentation of information

2. [X] Claims Nos.: 1-28, 40-54
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-4,14,15,17,22-24,40,41,44-46(all entirely) 47-50(all partially)

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-4,14,15,17,22-24,40,41,
44-46 (all entirely) 47-50 (all partially)

Invention 1:

A method of prediciting at least one toxic effect of a compound; a method of predicting the progression of a toxic effect of a toxic effect of a compound; a method of prediciting the hepatotoxicity of a compound; a method of identifying an agent that modulates the onset or progresion of a toxic response, wherein all said methods comprising detecting the expression level of the BTG1 gene and of the sat-1 gene; a set of at least two probes specific for the sat-1 gene or the BAT1 gene; a solid support comprising at least two said probes; a kit comprising said solid support.

2. Claims: 51-54 (all entirely)

Invention 2:

A method of identifying an agent that modulates at least one activity of a protein encoded by the sat-1 gene or the BAT1 gene.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-28, 40-54

1. Present claims 1-28, 40-54 relate to an extremely large number of possible products and methods. In fact, the claims contain so many possible options, variables and permutations that a lack of clarity and conciseness within the meaning of Art. 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Table 1 lists a vast number of genes exceeding 1000. The determination of their exact number amounts to an undue burden, in particular as different genes are listed several times. Tables 2 and 3 do not mention any genes, but refer to genes by either a generic ID no. or a comparison code. Again, it would amount to an undue burden to determine the genes referred to. Even if the identity and number of genes could be determined unambiguously, said claims still relate to a vast number of permutations. Consequently, a search was considered only possible for those parts of the application which do appear to be clear and concise, namely products and methods referring to the first two genes mentioned in Table 1 identifiable by GenBank Acc ID NM_017258 (rat BTG1 gene) and NM_022287 (rat sat-1 gene).

2. The term "cellular pathway" used in claim 5 is unclear, thereby rendering the definition of the subject-matter of said claim unclear (Art. 6 PCT). Although some of the genes listed in Table 1 are assigned to a cellular pathway indicated by a generic name, the definition of said indicated pathway is unclear. As dependent claim 16 does not specifiy said term, the same applies to said claim. Consequently, claims 5 and 16 were not searched.

3. In conclusion, only claims 1-4, 14, 15, 17, 22-24, 40, 41, 44-54 were considered searchable insofar as relating to the above genes, whereas claims 5-13, 16, 18-21, 25-28, 42, and 43 which relate to more genes were not considered searchable.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 01/23872

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0012760 A	09-03-2000	US 6403778 B	11-06-2002
		US 6160105 A	12-12-2000
		US 6160104 A	12-12-2000
		AU 6022299 A	21-03-2000
		CA 2340589 A	09-03-2000
		EP 1108067 A	20-06-2001
		JP 2002523112 T	30-07-2002